

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷: C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00	A2	(11) International Publication Number: WO 00/08187 (43) International Publication Date: 17 February 2000 (17.02.00)
(21) International Application Number: PCT/EP99/05652 (22) International Filing Date: 4 August 1999 (04.08.99) (30) Priority Data: 98202634.6 4 August 1998 (04.08.98) EP (71) Applicant (for all designated States except US): VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijnvischestraat 120, B-9052 Zwij- naarde (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): LEE, Jeong, Hée [KR/BE]; Spilmolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). (74) Agent: DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS (57) Abstract <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant
5 molecular biology. In particular, the invention relates to improvements of crop
productivity of useful plants. One of the major limitations of crop productivity is the
effect of environmental stress conditions on plant growth and development. An
important goal of molecular biology is the identification and isolation of genes that can
provide resistance or tolerance to such stresses. For agriculture, the creation of
10 transgenic plants containing such genes provides the potential for improving the stress
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on
the growth of plants and the productivity of crops. The physiological response to these
stresses arises out of changes in cellular gene expression. Expression of a number of
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be
classified into two groups: those that directly protect against environmental stresses
and those that regulate gene expression and signal transduction in the stress
response. The first group includes proteins that likely function by protecting cells from
20 dehydration, such as the enzymes required for biosynthesis of various
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,
Bray et al., 1997). The second group of gene products includes transcription factors,
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the
30 hypothesis that the genetic information for tolerance to environmental stress conditions
exists in all higher plants. In glycophytes, this information would only be expressed in
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of
35 evidence also demonstrate that even mild environmental stress conditions throughout
the growth season have a negative impact on plant growth and crop productivity. It is

CONFIRMATION COPY

for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by a non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO₂ etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride,
15 calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

10 The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996), Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

15 The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid
30 comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DBF2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

(a) SEQ ID NO 5, or the complementary strand thereof;

(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

(d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

10

Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given polynucleotide sequence.

15

20

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

25

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

30

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially
5 identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be
10 produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et
15 al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide
20 encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at
25 least part of the sequence of any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a
30 recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least
35 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5 The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10 The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression in these systems.

15 The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress of said plant.

20 The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

25 The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

30 Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced
5 tolerance or resistance to environmental stress, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

10 (a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

20 (b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified
25 from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said
30 method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

- (a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, Pannisetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one or more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardia glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

20 The present invention also relates to the cloning of the genomic counterpart of any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

 The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region
5 under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this
10 region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb
15 long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic
20 acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical
25 composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or
30 resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for
35 plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references
5 mentioned herein are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37° C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H₂O₂ (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H₂O₂ (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H₂O₂ (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut für Züchtungsforschung, Köln, Germany).

5 Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to
10 OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

 Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during
15 plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown
20 in b and d using a PhosphorImager (Molecular Dynamics).

 Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
25 section) upon applying a salt stress of 200 mM NaCl overnight.

 Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
30 section) upon applying an osmotic stress induced by 20% PEG overnight.

 Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C.

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C.

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H₂O₂, or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H₂O₂ (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C. For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

25	+	:	similar growth to the DY wild type cells;
	++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
	+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
30	++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

35

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H₂O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)₁₄-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the *Arabidopsis* cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected *Arabidopsis* cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected *Arabidopsis* cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD₆₀₀ at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

Example 3. Characterization of *At-DBF2*.

At-DBF2, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward et al. 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks et al. (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

10
15

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

20

Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

25

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

30
35

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive
5 role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

10 **Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.**

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-BDF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the
15 overexpression of both *DBF2* and *At-DBF2* (Figure 4).

Example 6. *At-DBF2* is cell cycle regulated.

DBF2 expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4
20 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S
25 phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases
30 until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*, 1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the *gfp* receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-CaMVter. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of
5 the three lines at least five times higher than the fresh weight of the control transgenic calli.

Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2,
10 p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation
15 experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight
20 incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

25 To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For
30 each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASA+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance
35 germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l⁻¹ sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol :chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N ; Amersham, little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 µg³ denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA.

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR ; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

Tabel 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dictyostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent - kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 - sequence	107	+++	++++
unknown	chromosome 4 - sequence	109	+	++++
unknown	chromosome 5 - sequence	111	++++	+++
unknown	chromosome 5 - sequence	113	++++	++
unknown	chromosome 5 - sequence	115	++++	++++
unknown	chromosome 5 - sequence	117	+	++++
unknown	chromosome 5 - sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
------------	--	-----	------	------

TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF
THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	Aleurone	Lanahan <i>et al.</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin β -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	http://salus.medium.edu/mmg/tierney/html
chalcone synthase (<i>chsA</i>)	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/gwrdc/csh95-1.html
<i>rbcS-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmg/tierney/html
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
β -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.medium.edu/mm/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.medium.edu/mm/tierney/html
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczynski <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
LEAFY	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
CLAVATA1	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
Blz2	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate synthase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

REFERENCES

- Adams et al. (1983), J. Am. Chem. Soc. 105:661
- Aerne et al. (1998). Molecular Biology of the Cell, vol 9, 945-956.
- Bray et al. (1997), Plant responses to water deficit. Trends Plant Sci 2, 48-54
- 5 Carruthers et al. (1982), Cold Spring Harbor Symp. Quant. Biol. 47:411-418
- Capecchi (1989), Science 244:1288-1292
- Deblaere et al. (1985), Efficient octopine Ti plasmid-derived vectors for Agrobacterium-mediated gene transfer to plants, Nucl. Acids Res. 13, 4777-4788.
- De Greve et al. (1982), J. Mol. Appl. Genet. 1(6):499-511
- 10 Dellaporta et al. (1983), A plant DNA miniprep, version II. Plant Mol. Biol. Rep. 1, 19-22
- Evans et al. (1983), Protoplasts Isolation and Culture, Handbook of Plant Cell Culture, pp. 124-176
- Fowden et al. (1993), Plant Adaptation to Environmental Stress; ISBN: 0412490005
- 15 Fraley et al. (1983), Proc. Natl. Acad. Sci USA 80:4803
- Fromm et al. (1985), Proc. Natl. Acad. Sci. USA 82:5824
- Gietz and Schietel, (1995) Methods in Molecular and Cellular Biology, 5, 255-269.
- Grillo et al (1996), Physical Stresses in Plants: Genes and Their Products for Tolerance. Springer Verlag; ISBN: 3540613471
- 20 Hanks et al. (1988). Science, 241, 42-52.
- Hansen et al. (1999), Trends in plant science reviews, Vol 4, No 6, 226-231
- Haring et al. (1991), Plant Mol. Biol. 16:449-469
- Haro et al. (1991). FEBS Lett, 291, 189-191.
- Haseloff et al. (1988), Nature 334:585-591
- 25 Hemmerlin and Bach (1998). Plant Journal 14 (1) 65-74 Johnston et al. (1990). Mol and Cell Biol 10, no 4, 1358-1366
- Herrera - Estrella (1983), Nature 303:209-213
- Holmberg & Bülow (1998), Improving stress tolerance in plants by gene transfer. Trends Plant Sci. 3, 61-66
- 30 Horsch et al., 1984), Science 233:496-498
- Hull and Howell (1987), Virology 86:482-493
- Ingram et al. (1996), The molecular basis of dehydration tolerance in plants. Ann. Rev. Plant Physiol. Plant Mol. Biol. 47, 377-403
- Innis et al. (1990), A guide to methods and applications, Academic Press, San Diego

- Jones et al (1989), *Plants Under Stress: Biochemistry, Physiology and Ecology and Their Application to Plant Improvement* (Society for Experimental Biology Seminar Serie), Cambridge Univ. Pr. (Short); ISBN: 0521344239
- Johnston et al. (1995)
- 5 Kasuga et al. (1999), *Nature Biotechnology* 17, 287-291
- Klee et al. (1987), *Ann. Rev. of Plant Phys.* 38:467-486
- Klein et al. (1987), *Nature* 327:70-73
- Komamitsky et al. (1998), *Mol and Cell Biol.* 18, no.4, 2100-2107
- Lee et al (1999). *Proc. Nat. Acad. Sci. USA* 1996, 5873-5877
- 10 Meyer et al. (1987), *Nature* 330:677
- Millward et al. (1995). *Proc. Nat. Acad. Sci. USA*, 92, 5022-5026.
- Nagata et al. (1992). *Int. Rev. Cytol.*, 132, 1-30
- Napoli et al. (1990), *The Plant Cell* 2:279-289
- Needleman and Wunsch (1970), *Mol. Biol.* 48:443
- 15 Nilsen et al (1996), *The Physiology of Plants Under Stress; Abiotic Factors*. ISBN: 047131526
- Odell et al. (1985), *Nature* 313:482-493
- Paszkowski et al. (1984), *EMBO j.* 3:2717-2722
- Pearson and Lipman (1988), *Proc. Natl. Acad. Sci. (USA)* 85:2444
- 20 Peassarakli et al, *Handbook of Plant and Crop Stress*. ISBN: 0824789873
- Raton (1985), *Binding, Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press
- Reicheld et al. (1995). *Plant Journal* 7 (2) 245-252
- Sambrook (1989), *Molecular cloning, a laboratory manual*, Cold Spring Harbor Press,
- 25 7.52.
- Shaul et al. (1996). *PNAS* 93,4868-4872
- Shinozaki et al. (1996), *Molecular responses to drought and cold stress*, *Curr. Opin. Biotechnol.* 7, 161-167
- Shinozaki et al. (1997), *Gene expression and signal transduction in water-stress response*. *Plant Physiol.* 115, 327-334
- 30 Shinozaki et al. (1999), *Drought, Salt, Cold and Heat Stress: Molecular Responses in Higher Plants* (Biotechnology Intelligence Unit); ISBN: 1570595631
- Schuller et al. (1994). *Embo Journal*, 13, 4382-4389.
- Smith and Waterman (1981), *Adv. Appl. Math.* 2:482

- Tomashow (1994), *Arabidopsis* (eds Meyrowitz, E & Somerville, C, 807-834 (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1994)
- Toyn and Johnston, (1994). *Embo Journal*, 13, 1103-1113.
- Verbruggen et al. (1993). *Plant Phys.* 103, 771-781
- 5 Walbot (1992), *Ann. Rev. Plant Mol. Biol.* 43:49-82
- Weising et al; (1988), *Ann; Rev. Genet.* 22:421-477
- Stalker, *Science* 242 (1988), 419
- Vaek, *Plant Cell* 5 (1987), 159-169
- Powell, *Science* 232 (1986), 738-743
- 10 Pappu, *World Journal of Microbiology & Biotechnology* 11 (1995), 426-437
- Lawson, *Phytopathology* 86 (1996) 56 suppl.
- Van Camp, *Biotech.* 12 (1994), 165-168
- Oeller, *Science* 254 (1991), 437-439
- Stark, *Science* 242 (1992), 419
- 15 Visser, *Mol. Gen. Genet.* 225 (1991), 289-296
- Voelker, *Science* 257 (1992), 72-74
- Poirer, *Science* 256 (1992), 520-523
- Meyer, *Nature* 330 (1987), 667-678
- Duering, *Molecular Breeding* 2 (1996), 297-305
- 20 Strittmatter, *Bio/Technology* 13 (1995), 1085-1089
- Estruch, *Nature Biotechnology* 15 (1997), 137-141
- An, et al., *Plant Physiol.* 88: 547, 1998.
- Albani, et al., *Plant Mol. Biol.* 15: 605, 1990.
- Albani, et al., *Plant Mol. Biol.* 16: 501, 1991.
- 25 Arnoldo, et al., *J. Cell. Biochem., Abstract No. Y101*, 204, 1992.
- Baltz, et al., *The Plant J.* 2: 713-721, 1992.
- Baszczynski, et al., *Nucl. Acid Res.* 16: 4732, 1988.
- Baszczynski, et al., *Plant Mol. Biol.* 14: 633, 1990.
- Bhattacharyya-Pakrasi, et al, *The Plant J.* 4: 71-79, 1992.
- 30 Cejudo, F.J., et al. *Plant Molecular Biology* 20:849-856, 1992.
- Conkling, et al., *Plant Physiol.* 93: 1203, 1990.
- Crowell, et al., *Plant Mol. Biol.* 18: 459-466, 1992.
- Cummins, et al., *Plant Mol. Biol.* 19: 873-876, 1992
- Ellis, et al., *Plant Mol. Biol.* 10: 203-214, 1988.
- 35 Gordon, et al., *J. Exp. Bot.* 44: 1453-1465, 1993.

- Grimes, *et al.*, *The Plant Cell* 4:1561-1574, 1992.
- Hamilton, *et al.*, *Plant Mol. Biol.* 18: 211-218, 1992.
- Kosugi *et al.*, Upstream sequences of rice proliferating cell nuclear antigen (PCNA) gene mediate expression of PCNA-GUS chimeric gene in meristems of transgenic tobacco plants, *Nucleic Acids Research* 19:1571-1576, 1991.
- Kosugi S. and Ohashi Y, PCF1 and PCF2 specifically bind to cis elements in the rice proliferating cell nuclear antigen gene, *Plant Cell* 9:1607-1619, 1997.
- Lam, E. *et al.*, *The Plant Cell* 2: 857-866, 1990.
- Lanahan, M.B., *et al.*, *Plant Cell* 4:203-211, 1992.
- Liu *et al.*, *Plant Mol. Biol.* 153:386-395, 1991.
- Matzke *et al* *Plant Mol Biol*, 14(3):323-32 1990
- Nasrallah, *et al.*, *Proc. Natl. Acad. Sci. USA* 85: 5551, 1988.
- Nilsson *et al.*, *Physiol. Plant.* 100:456-462, 1997
- Oppenheimer, *et al.*, *Gene* 63: 87, 1988.
- Pathirana, *et al.*, *Plant Mol. Biol.* 20: 437-450, 1992.
- Pearson, *et al.*, *Plant Mol. Biol.* 18: 235-245, 1992.
- Scofield, *et al.*, *J. Biol. Chem.* 262: 12202, 1987.
- Simon, *et al.*, *Plant Mol. Biol.* 5: 191, 1985.
- Stalberg, *et al*, *Planta* 199: 515-519, 1996.
- Suzuki *et al.*, *Plant Mol. Biol.* 21: 109-119, 1993.
- Skriver, K., *et al. Proc. Natl. Acad. Sci. (USA)* 88: 7266-7270, 1991.
- Takaiwa, *et al.*, *Mol. Gen. Genet.* 208: 15-22, 1986.
- Takaiwa, *et al.*, *FEBS Letts.* 221: 43-47, 1987.
- Tingey, *et al.*, *EMBO J.* 6: 1, 1987.
- Trick, *et al.*, *Plant Mol. Biol.* 15: 203, 1990.
- Tucker *et al.*, *Plant Physiol.* 113: 1303-1308, 1992.
- Van der Meer, *et al.*, *Plant Mol. Biol.* 15, 95-109, 1990.
- Van der Zaal, *et al.*, *Plant Mol. Biol.* 16, 983, 1991.
- Vicente-Carbajosa *et al.*, *Plant J.* 13: 629-640, 1998.
- Weigel *et al.*, *Cell* 69:843-859, 1992.
- Yamamoto *et al.*, *Plant Cell Physiol.* 35:773-778, 1994.
- Yang, *et al.*, *The Plant J.* 3: 573-585.
- Clarke *et al.* (1992), *Plant Molecular Biology Reporter* Volume 10(2), 178-189
- Ausubel *et al.* (1994),
- Zhu *et al.* (1997),

- Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
- Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
- Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
- Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
- Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
- Barros et al., Plant Mol Biol, 19(4): 665-75, 1992.
- Marrs et al., Dev Genet., 14(1): 27-41, 1993.
- Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
- Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
- Ouellet et al., FEBS Lett. 423, 324-328 (1998)
- Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997
- Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994
- Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998
- Schneider et al., Plant Physiol, 113(2): 335-45, 1997
- Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
- Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993
- Valvekens et al. (1988)
- Porta et al. (1996), Mol Biol, 5(3):209-21

Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
 - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
 - (a) SEQ ID NO 1, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of
- 20 (a) to (c).

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 25 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to
35 environmental stress conditions.

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- 5
- (a) SEQ ID NO 5, or the complementary strand thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - 10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or
120.

13. A method for producing a plant with enhanced tolerance or resistance to
environmental stress, said method comprising transiently introducing into a plant
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of
claims 2 to 10 which is expressed in an amount effective to confer enhanced
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to
30 environmental stress, said method comprising stably introducing into a plant cell a
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2
to 10 which is expressed in an amount effective to confer enhanced tolerance or
resistance to environmental stress.

35

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.
- 5 16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.
- 10 17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.
- 15 18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
 - a plant expressible promoter, whereby said
- 20 polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 25 19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:
- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly
- 30 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:
a polynucleic acid according to or as defined in any of claims 2 to 10, and,
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
- 30 24. The recombinant polynucleic acid of claim 21 comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

At-DBF2	DAGY FDDFWNEADIAKYADVFNSGCCRTALVODSAVSSKLVGFTFRHRNKGQSSGMLFNGLEHSDPFSTFY	528
DBF2	DAGY FDDFTSEADMAKYADVFKRQDKLTANVODSAVSSKLVGFTFRHRNKGQSSGILFNGLEHSDPFSTFY	572

FIGURE 1 A

2/15

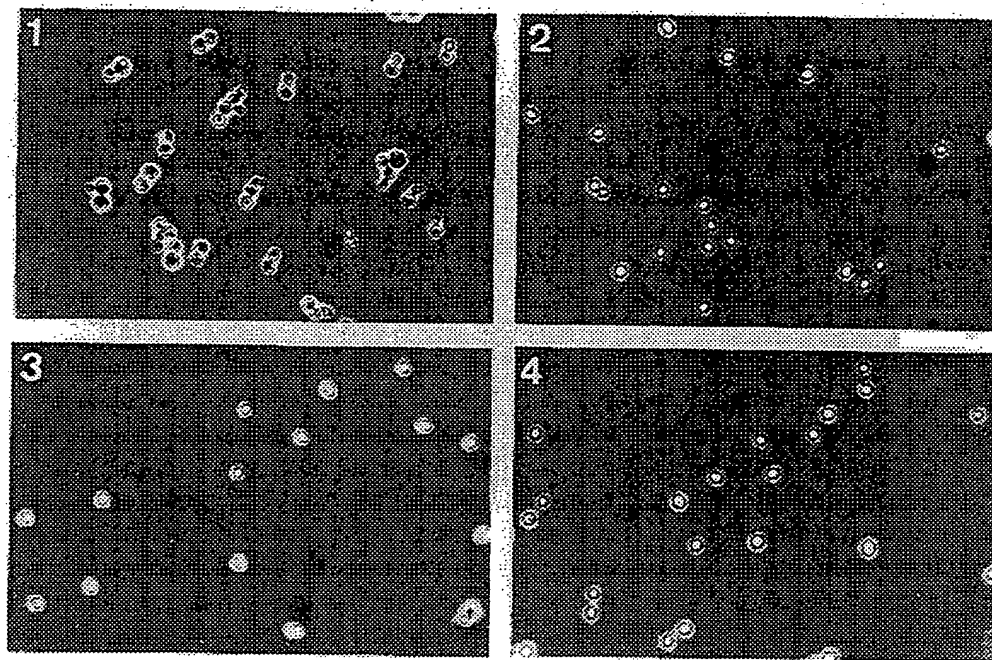


FIGURE 1B

3/15

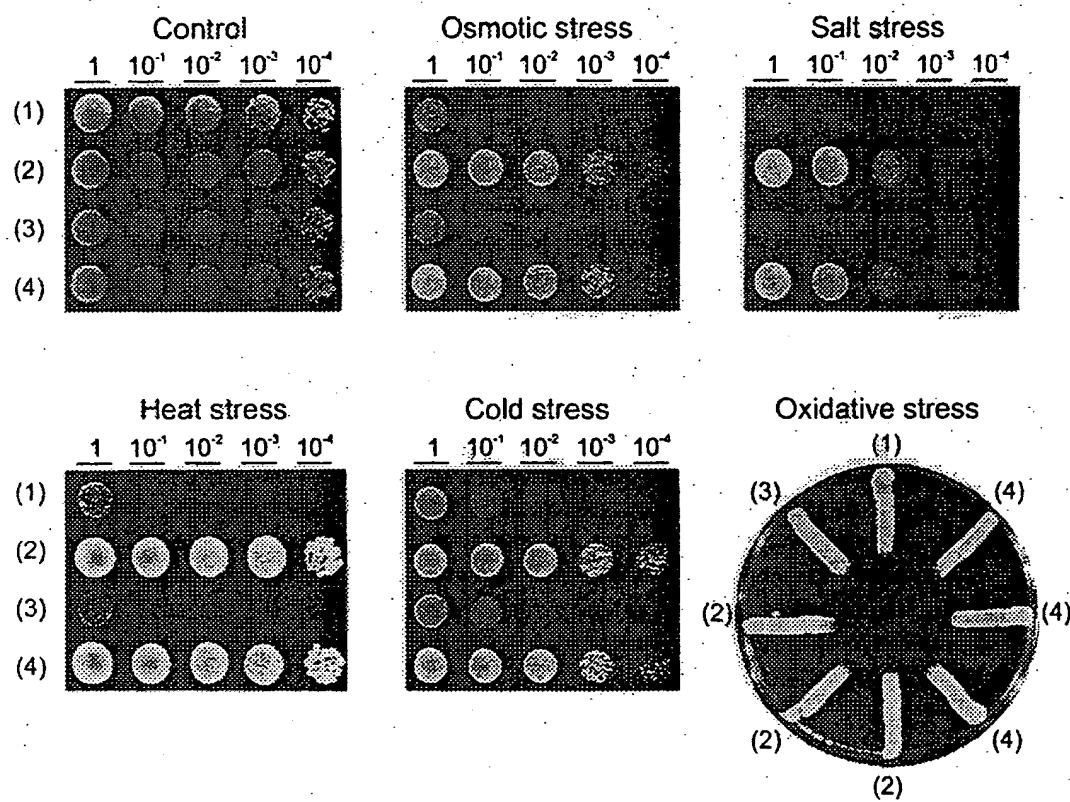


FIGURE 2

4/15

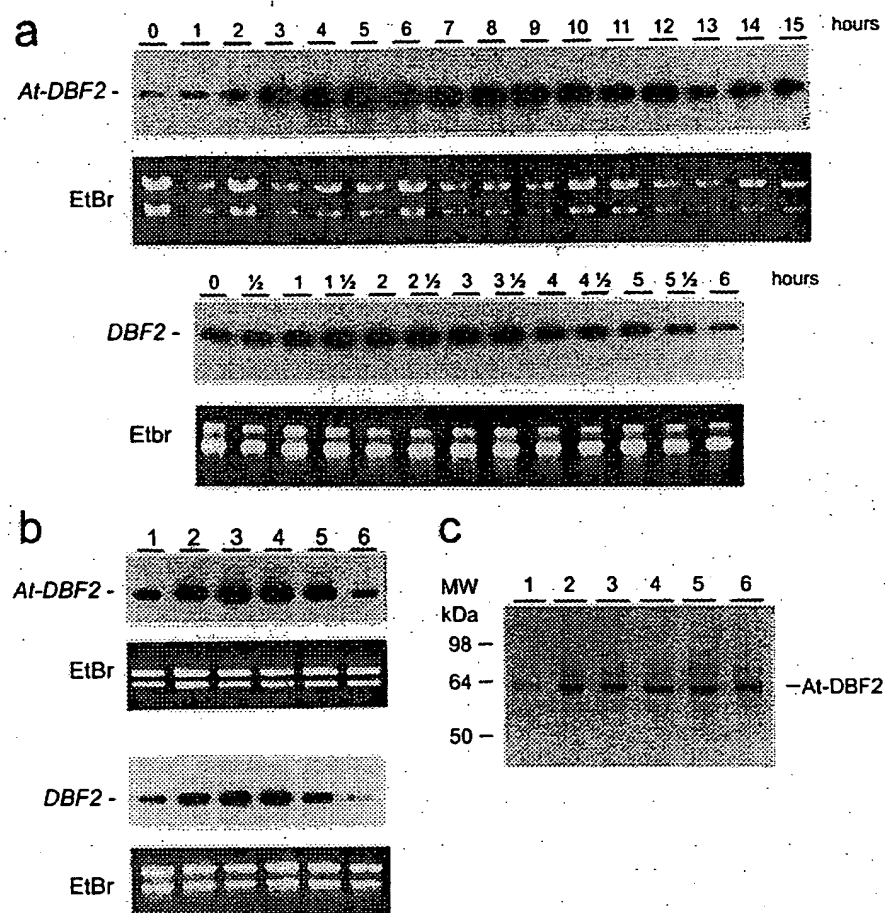


FIGURE 3

5/15

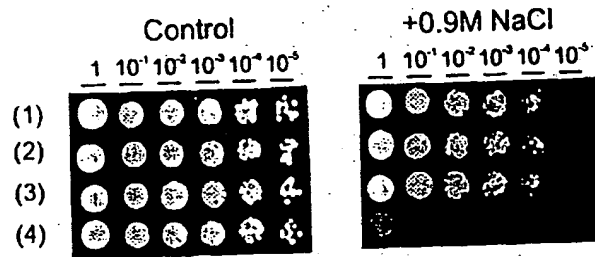


FIGURE 4

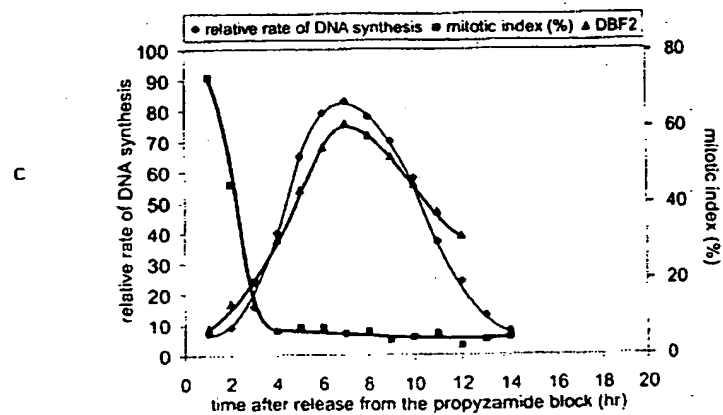
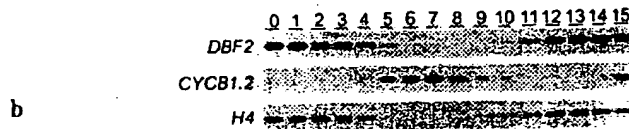
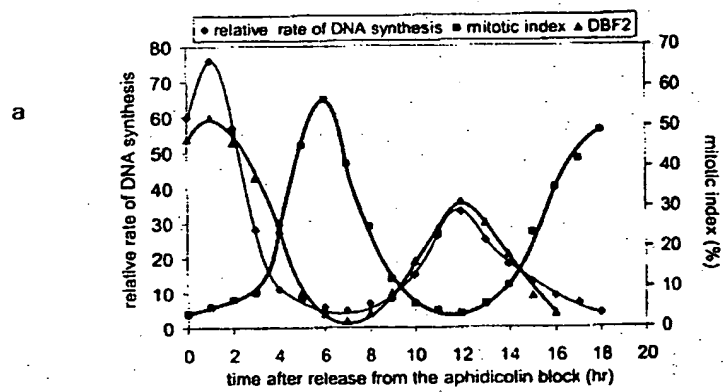


FIGURE 5

6/15

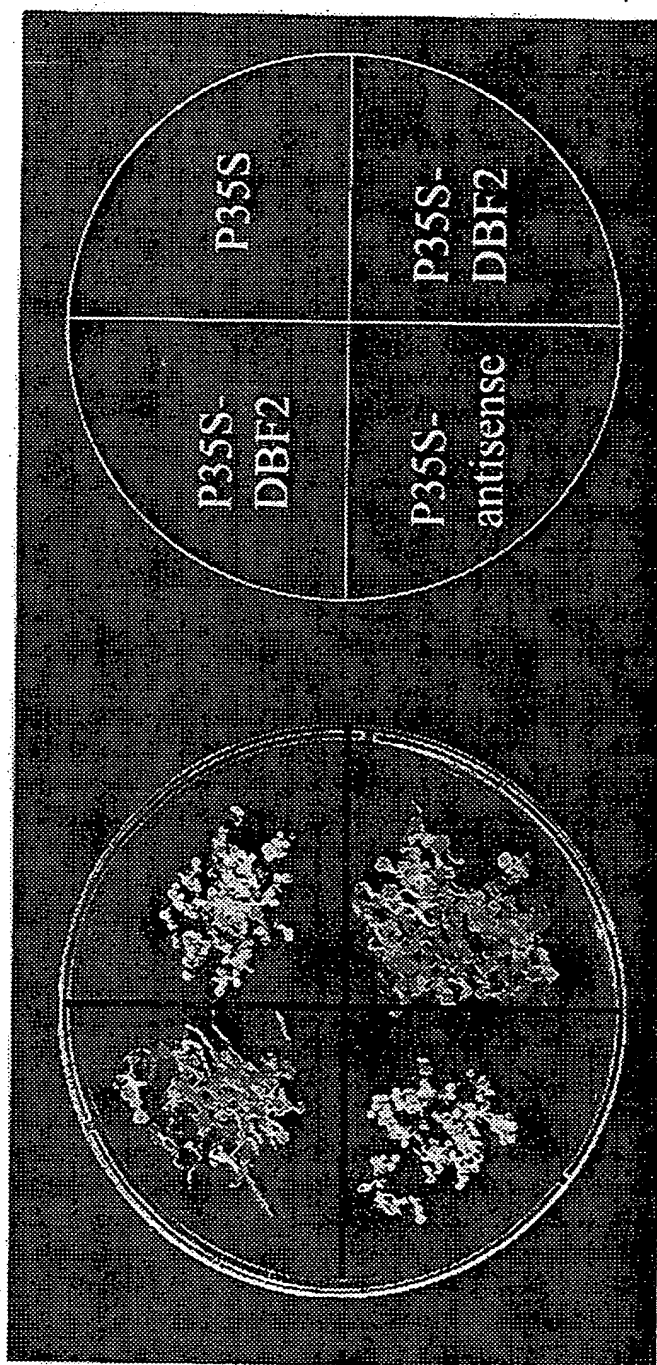


FIGURE 6

7/15

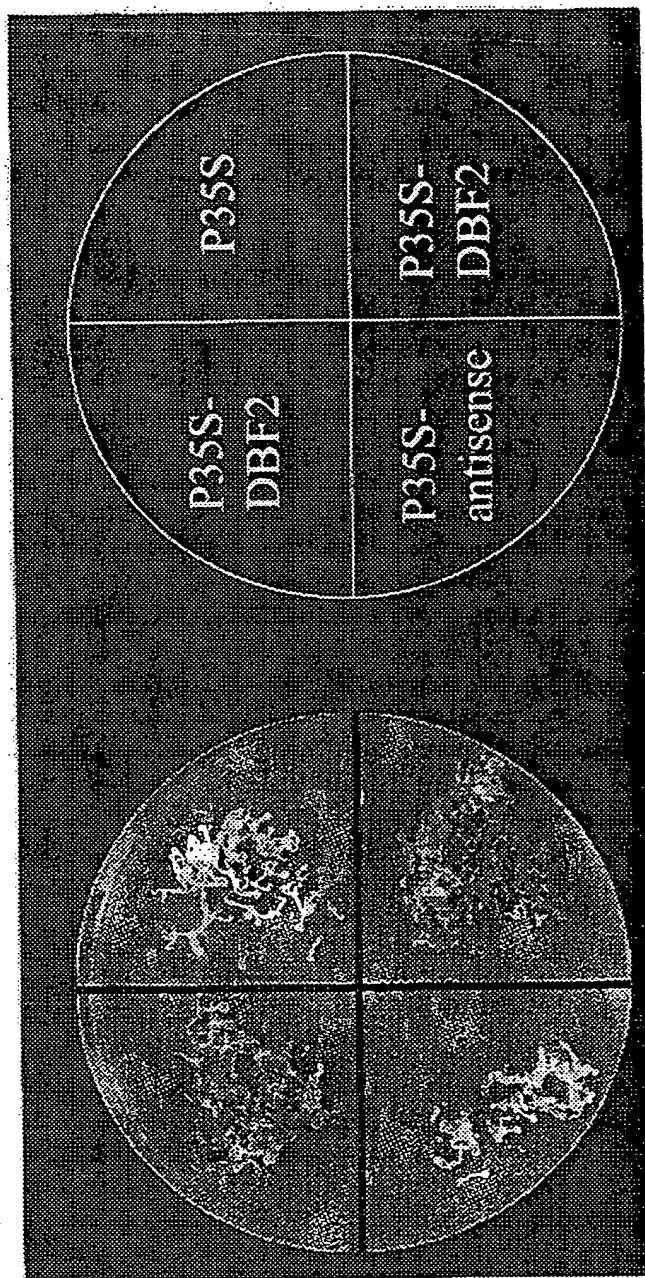


FIGURE 7

8/15

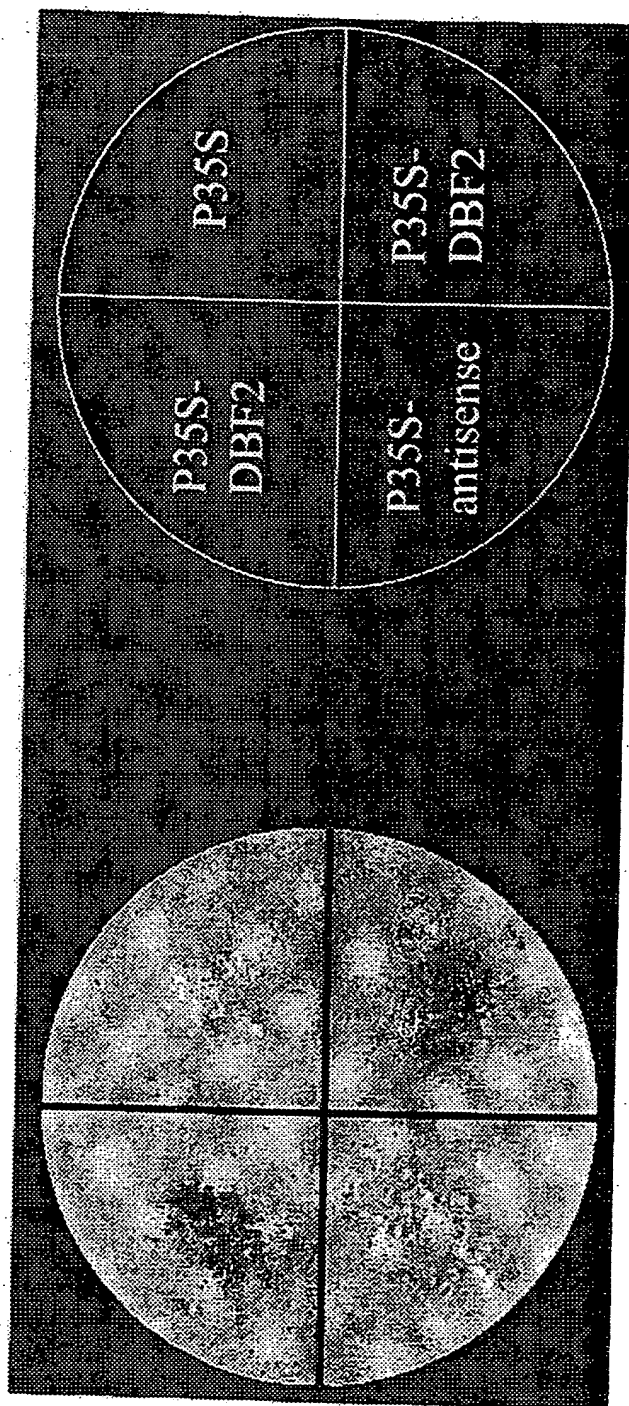


FIGURE 8

9/15

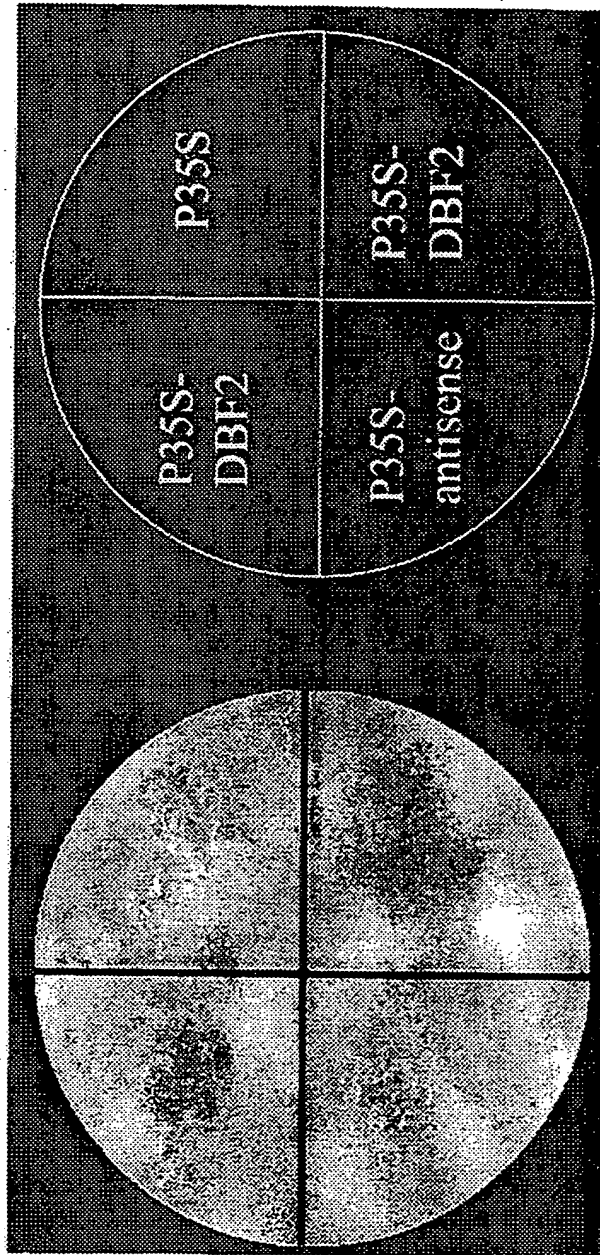


FIGURE 9

10/15

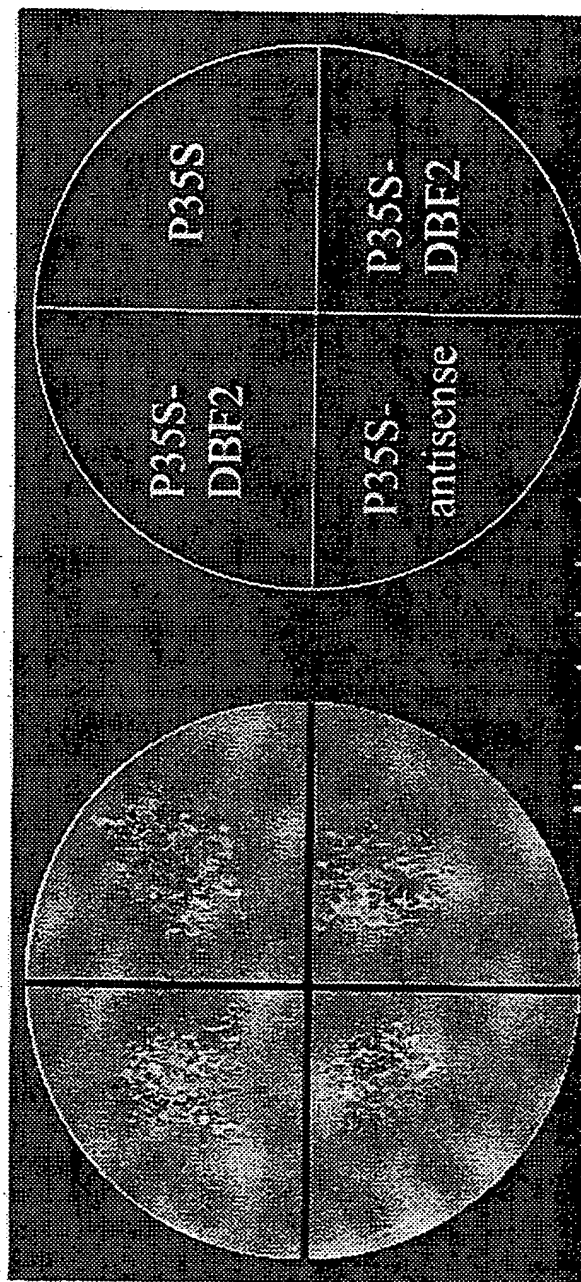


FIGURE 10

11/15

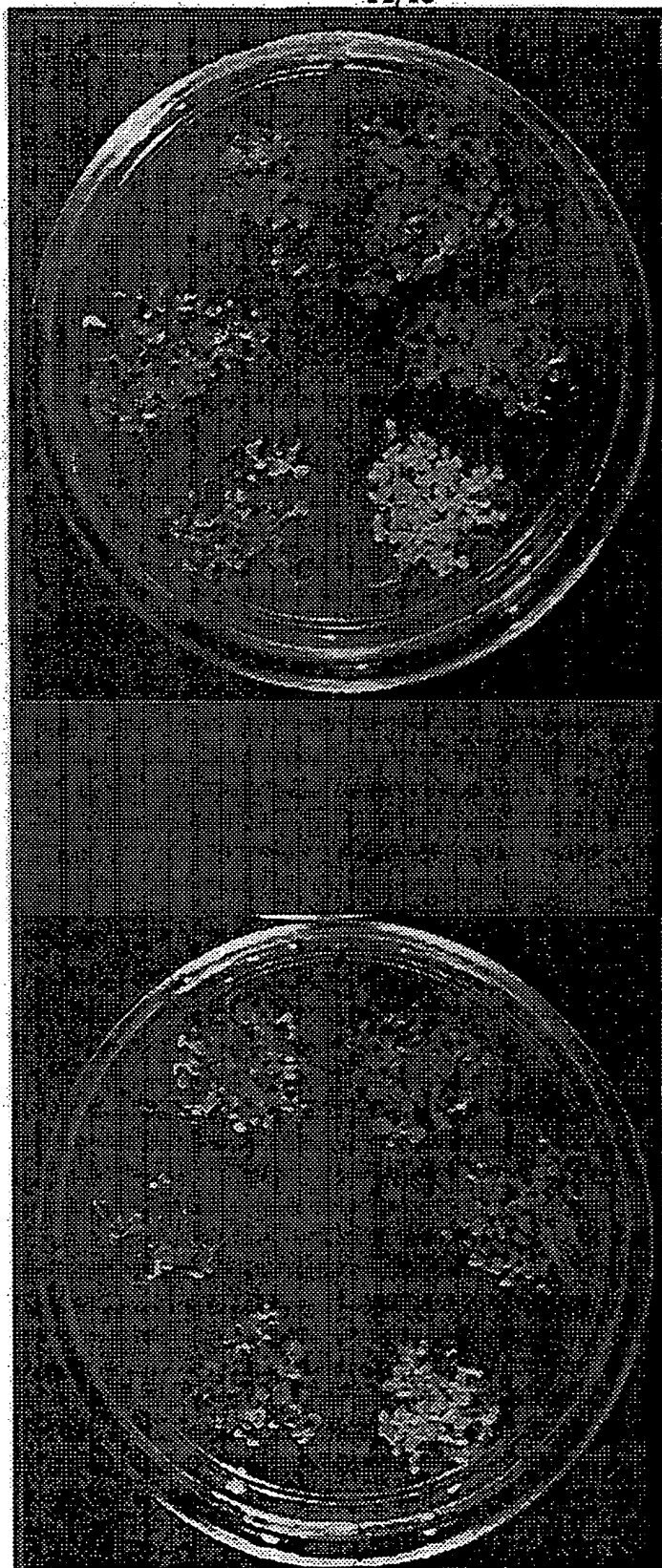


FIGURE 11

12/15

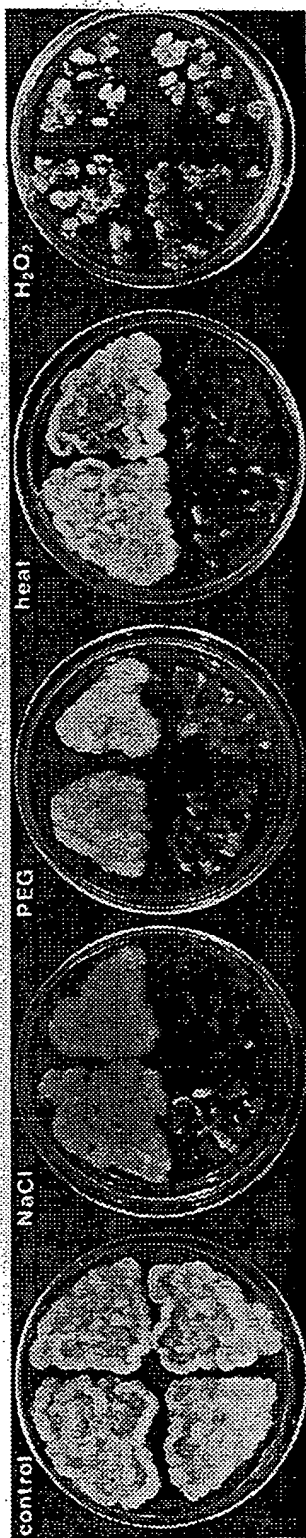


FIGURE 12A

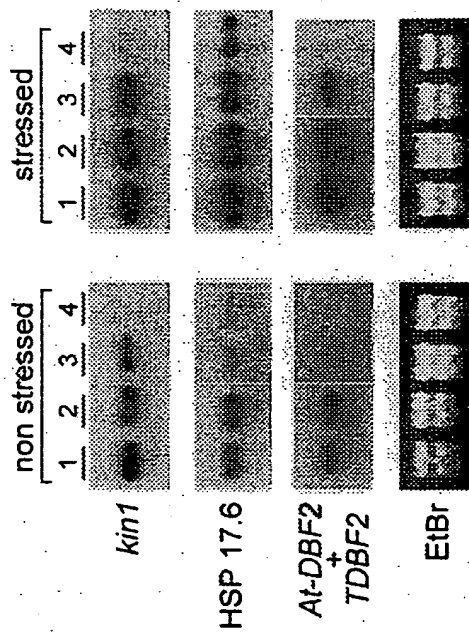


FIGURE 12c

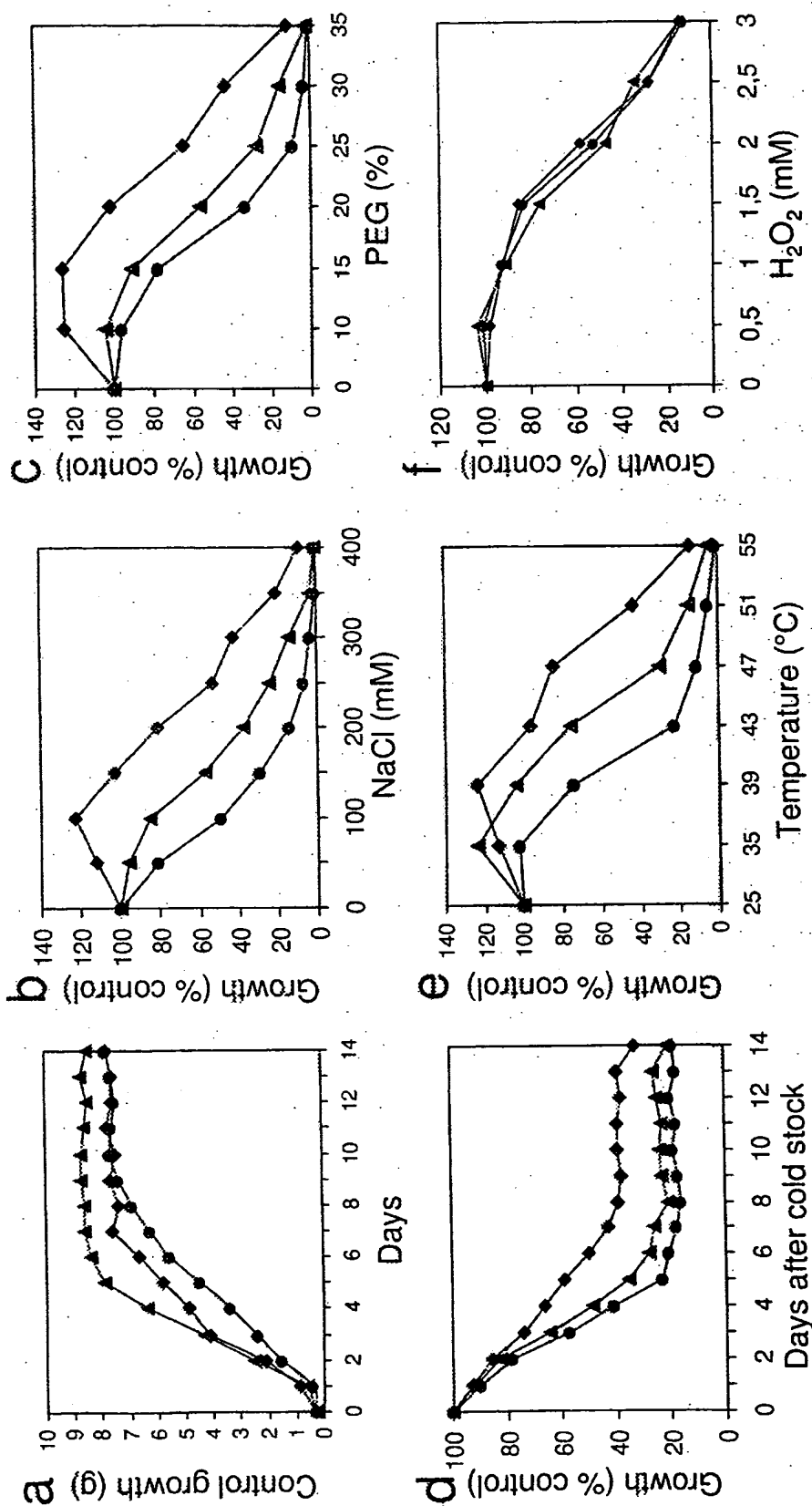


FIGURE 12B

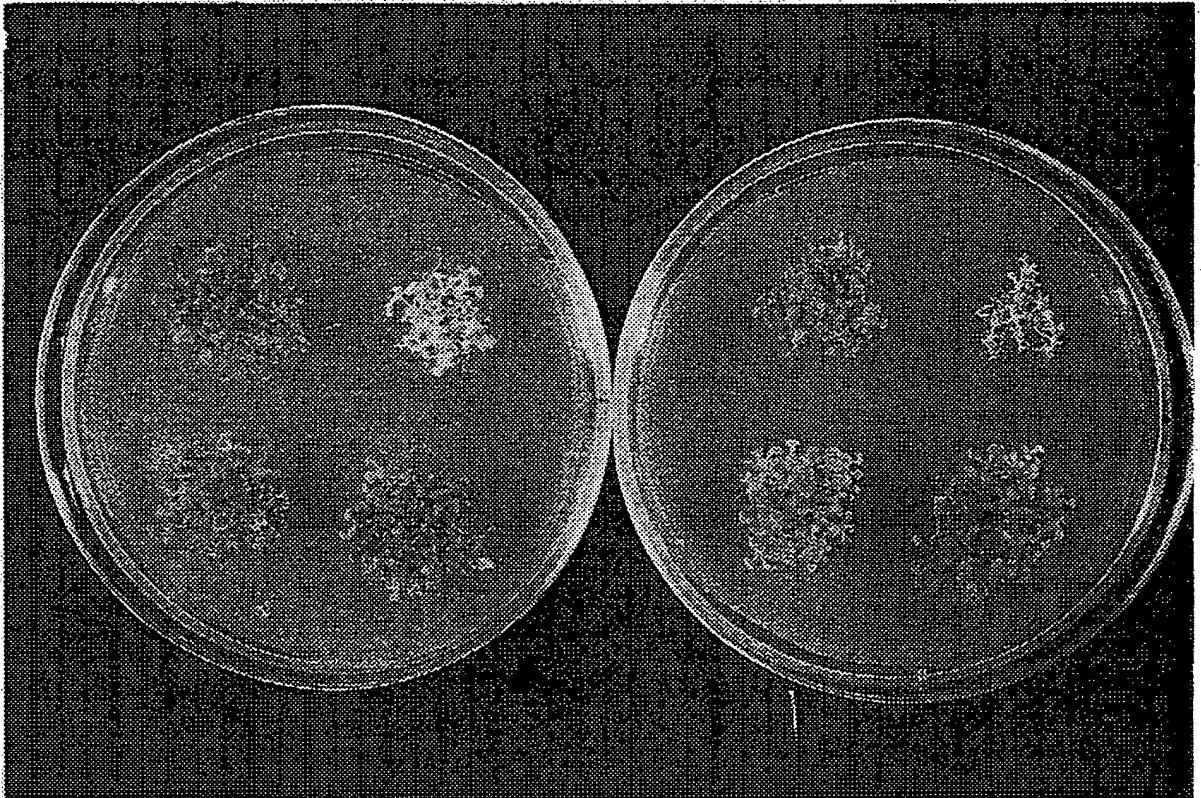


FIGURE 13

15/15

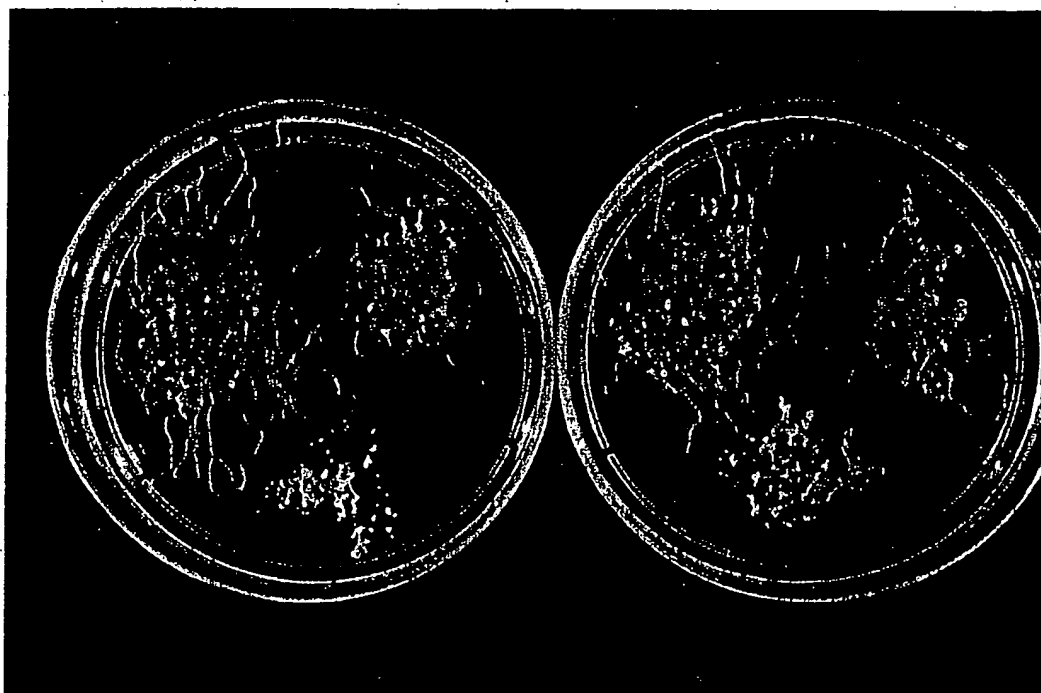


FIGURE 14

SEQUENCE LISTING

<110> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE

<120> Genes involved in tolerance to environmental stress

<130> VIB-14-NV/OSMO

<140>

<141>

<150> 98202634.6

<151> 1998-08-04

<160> 126

<170> PatentIn Ver. 2.1

<210> 1

<211> 1909

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (40)..(1626)

<400> 1

```

cggtagcctg actgctggat tggcctgctg ctgacaatt atg gcg ggt aac atg      54
                                   Met Ala Gly Asn Met
                                   1           5

tcg tgt tta agc acg gac gga cac ggg acc cct ggc ggt tca ggg cat      102
Ser Cys Leu Ser Thr Asp Gly His Gly Thr Pro Gly Gly Ser Gly His
              10              15              20

ttc ccc aat cag aac cta acg aaa aga aga acg cgt cca gcg ggt atc      150
Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
              25              30              35

aac gac tcg cct tcg ccg gtg aaa tgc ttt ttt ttc ccc tat gaa gac      198
Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe Phe Pro Tyr Glu Asp
              40              45              50

acc tcc aac acg tca tta aag gaa gtg tcc cag ccc acg aaa tac agt      246
Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln Pro Thr Lys Tyr Ser
              55              60              65

tcc aat tcc cct cca gtc agc ccg gca att ttt tat gag agg gcg acg      294
Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
              70              75              80              85

tcg tgg tgc acg caa agg gtg gtg agt ggg agg gca atg tac ttt cta      342
Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg Ala Met Tyr Phe Leu
              90              95              100

gaa tat tat tgc gat atg ttc gat tat gta att agc agg aga caa cgc      390

```

Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile Ser Arg Arg Gln Arg	
105 110 115	
acg aaa cag gtc cta gag tat ctg cag cag caa agc caa ctt ccg aat	438
Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln Ser Gln Leu Pro Asn	
120 125 130	
tct gac cag atc aag ctc aac gaa gag tgg tcc tcc tat tta cag aga	486
Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser Ser Tyr Leu Gln Arg	
135 140 145	
gag cat cag gtt ttg tcg aaa aga agg ttg aag cca aaa aac aga gac	534
Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys Pro Lys Asn Arg Asp	
150 155 160 165	
ttt gaa atg att aca caa gta ggt caa ggt ggt tat ggg cat gtt tat	582
Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly Tyr Gly His Val Tyr	
170 175 180	
tta gcc aga aag aaa gac aca aaa gag gtg tgc gcc tta aaa att ttg	630
Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys Ala Leu Lys Ile Leu	
185 190 195	
aat aag aag cta ggt ttc aaa ctt aat ggt aca tgc cat gtt ttg acc	678
Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr Cys His Val Leu Thr	
200 205 210	
gag agg cag agt ctg act aca acg aga tcc gag acg atg gtg aag ctc	726
Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu Thr Met Val Lys Leu	
215 220 225	
cta agt ggg acg acc ccc gta ggc agt agg ggg atg gcg ata gaa agt	774
Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly Met Ala Ile Glu Ser	
230 235 240 245	
gag cta ggc ggt gac ttc cgt aca gaa agt ata gga cgt aga tgc ttg	822
Glu Leu Gly Gly Asp Phe Arg Thr Glu Ser Ile Gly Arg Arg Cys Leu	
250 255 260	
aaa agt ggc cat gcg aga ttc tat att agc gaa atg ttc tgt gcc gtc	870
Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu Met Phe Cys Ala Val	
265 270 275	
aac gag aaa cat ctt tta agt aaa acg gac agc aca atc tcc aac gaa	918
Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser Thr Ile Ser Asn Glu	
280 285 290	
gaa gat agt agc atc aac ata agg tta gaa aaa ttc aaa gac ctt ggg	966
Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys Phe Lys Asp Leu Gly	
295 300 305	
tac cca gcg ttg agc gag aaa tct atc gag gac agg agg aag ttg tac	1014
Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp Arg Arg Lys Leu Tyr	
310 315 320 325	
acc tgt ccg aac tcc atg gtt ggg tct ccg gac tac ata gcc tta gaa	1062
Thr Cys Pro Asn Ser Met Val Gly Ser Pro Asp Tyr Ile Ala Leu Glu	

330	335	340	
gtc ttg aga gga aag agg tac gag tat	acc gta gac tat tgg tgc ttg	1110	
Val Leu Arg Gly Lys Arg Tyr Glu Tyr	Thr Val Asp Tyr Trp Ser Leu		
345	350	355	
ggt tgt atg ctg ttt gag agc ttg gtc ggc tac acc ccc ttc agt ggc	1158		
Gly Cys Met Leu Phe Glu Ser Leu Val Gly Tyr Thr Pro Phe Ser Gly			
360	365	370	
tgc tgc acc aac gaa acg tat gcg atc agt cgt agc tgg aaa cag acg	1206		
Ser Ser Thr Asn Glu Thr Tyr Ala Ile Ser Arg Ser Trp Lys Gln Thr			
375	380	385	
ttg aat aga gcg aga cac gag gat ggg agg gcg gcg ttt tac aat agg	1254		
Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala Ala Phe Tyr Asn Arg			
390	395	400	
acg tgg gac ttg att acc aga cac agg gcc gac cta agc acg cgg acg	1302		
Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp Leu Ser Thr Arg Thr			
410	415	420	
aga tcc ttt gag cac gag gta aag atg agc tac ttc gcg gac atc ttg	1350		
Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr Phe Ala Asp Ile Leu			
425	430	435	
ttt aag gcc tta aga tcg ata att cca cct ttc aca ccc caa cta gac	1398		
Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe Thr Pro Gln Leu Asp			
440	445	450	
agc gag acc gat gcc ggt tat ttc gat gac ttt tgg aat gag gct gac	1446		
Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe Trp Asn Glu Ala Asp			
455	460	465	
ata gcc aaa tac gct gac gtc ttt aat agt cag tgc tgc cgt acg gct	1494		
Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln Cys Cys Arg Thr Ala			
470	475	480	
tta gtc gac gat tct gct gtt tct tct aaa ctt gtt ggg ttc acc ttc	1542		
Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu Val Gly Phe Thr Phe			
490	495	500	
cga cac aga aat ggt aaa cag ggt tcc agt ggt atg tta ttc aac ggg	1590		
Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly Met Leu Phe Asn Gly			
505	510	515	
cta gaa cac tca gac ccc ttc tca acc ttt tac tag taatcggcag	1636		
Leu Glu His Ser Asp Pro Phe Ser Thr Phe Tyr			
520	525		
cctgcagcct gccagctgc cagcctgcc tcgctgacg cctgccccag gatgcctctc	1696		
ctttggataa catgcctgc tccccatgc cttgctgcct cgcagcctga acgcctgcca	1756		
gagctcgcca gcctgcccag ctttgcgcc cagcctgcca gccttttttt aaacgctgaa	1816		
aaacgcctaa aaaaatcgaa ctttaaacgc ttttaaaacg gctgcccata aaaaaaagg	1876		

ttttttaata aaaaatcgta aaaaaaaaaa cgt

1909

<210> 2

<211> 528

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Ala Gly Asn Met Ser Cys Leu Ser Thr Asp Gly His Gly Thr Pro
1 5 10 15

Gly Gly Ser Gly His Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr
20 25 30

Arg Pro Ala Gly Ile Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe
35 40 45

Phe Pro Tyr Glu Asp Thr Ser Asn Thr Ser Leu Lys Glu Val Ser Gln
50 55 60

Pro Thr Lys Tyr Ser Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe
65 70 75 80

Tyr Glu Arg Ala Thr Ser Trp Cys Thr Gln Arg Val Val Ser Gly Arg
85 90 95

Ala Met Tyr Phe Leu Glu Tyr Tyr Cys Asp Met Phe Asp Tyr Val Ile
100 105 110

Ser Arg Arg Gln Arg Thr Lys Gln Val Leu Glu Tyr Leu Gln Gln Gln
115 120 125

Ser Gln Leu Pro Asn Ser Asp Gln Ile Lys Leu Asn Glu Glu Trp Ser
130 135 140

Ser Tyr Leu Gln Arg Glu His Gln Val Leu Ser Lys Arg Arg Leu Lys
145 150 155 160

Pro Lys Asn Arg Asp Phe Glu Met Ile Thr Gln Val Gly Gln Gly Gly
165 170 175

Tyr Gly His Val Tyr Leu Ala Arg Lys Lys Asp Thr Lys Glu Val Cys
180 185 190

Ala Leu Lys Ile Leu Asn Lys Lys Leu Gly Phe Lys Leu Asn Gly Thr
195 200 205

Cys His Val Leu Thr Glu Arg Gln Ser Leu Thr Thr Thr Arg Ser Glu
210 215 220

Thr Met Val Lys Leu Leu Ser Gly Thr Thr Pro Val Gly Ser Arg Gly
225 230 235 240

Met Ala Ile Glu Ser Glu Leu Gly Gly Asp Phe Arg Thr Glu Ser Ile
245 250 255

Gly Arg Arg Cys Leu Lys Ser Gly His Ala Arg Phe Tyr Ile Ser Glu
 260 265 270
 Met Phe Cys Ala Val Asn Glu Lys His Leu Leu Ser Lys Thr Asp Ser
 275 280 285
 Thr Ile Ser Asn Glu Glu Asp Ser Ser Ile Asn Ile Arg Leu Glu Lys
 290 295 300
 Phe Lys Asp Leu Gly Tyr Pro Ala Leu Ser Glu Lys Ser Ile Glu Asp
 305 310 315 320
 Arg Arg Lys Leu Tyr Thr Cys Pro Asn Ser Met Val Gly Ser Pro Asp
 325 330 335
 Tyr Ile Ala Leu Glu Val Leu Arg Gly Lys Arg Tyr Glu Tyr Thr Val
 340 345 350
 Asp Tyr Trp Ser Leu Gly Cys Met Leu Phe Glu Ser Leu Val Gly Tyr
 355 360 365
 Thr Pro Phe Ser Gly Ser Ser Thr Asn Glu Thr Tyr Ala Ile Ser Arg
 370 375 380
 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala
 385 390 395 400
 Ala Phe Tyr Asn Arg Thr Trp Asp Leu Ile Thr Arg His Arg Ala Asp
 405 410 415
 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr
 420 425 430
 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe
 435 440 445
 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe
 450 455 460
 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln
 465 470 475 480
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu
 485 490 495
 Val Gly Phe Thr Phe Arg His Arg Asn Gly Lys Gln Gly Ser Ser Gly
 500 505 510
 Met Leu Phe Asn Gly Leu Glu His Ser Asp Pro Phe Ser Thr Phe Tyr
 515 520 525

<210> 3

<211> 695

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (94)..(564)

<400> 3

tattaagctt ggtaccgagc tcggatccac tagtaacggc cgccagtgtg ctggaattcg 60

gcacgagcaa gaaagttaac acaacagcta aga atg gat ttg gag ttt gga agg 114
 Met Asp Leu Glu Phe Gly Arg
 1 5

ttt cca ata ttt tca atc ctc gaa gac atg ctt gaa gcc cct gaa gaa 162
 Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
 10 15 20

caa acc gag aag act cgt aac aac cct tca aga gct tac atg cga gac 210
 Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
 25 30 35

gca aag gca atg gct gct aca cca gct gac gtt atc gag cac ccg gat 258
 Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
 40 45 50 55

gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
 Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
 60 65 70

cag gtc cag ata gag aac gag aac gtg ctt gtg gtg agt ggc aaa aga 354
 Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
 75 80 85

cag agg gac aac aag gag aat gaa ggt gtg aag ttt gtg agg atg gag 402
 Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
 90 95 100

agg agg atg ggg aag ttt atg agg aag ttt cag tta cct gat aat gca 450
 Arg Arg Met Gly Lys Phe Met Arg Lys Phe Gln Leu Pro Asp Asn Ala
 105 110 115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
 Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
 120 125 130 135

act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
 Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
 140 145 150

caa gtt caa gtc gct tga gtttgtttgt gatccgtgtt tttgtgtttt 594
 Gln Val Gln Val Ala
 155

aatgaatgta atcgataagc aactacctct tgggtgttcgt tgtaaaatga aataaaaata 654

gttttctctg ttcataaaaa aaaaaaaaaa aaaactcgag c 695

<210> 4
 <211> 156
 <212> PRT
 <213> Arabidopsis thaliana

<400> 4
 Met Asp Leu Glu Phe Gly Arg Phe Pro Ile Phe Ser Ile Leu Glu Asp
 1 5 10 15
 Met Leu Glu Ala Pro Glu Glu Gln Thr Glu Lys Thr Arg Asn Asn Pro
 20 25 30
 Ser Arg Ala Tyr Met Arg Asp Ala Lys Ala Met Ala Ala Thr Pro Ala
 35 40 45
 Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
 50 55 60
 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
 65 70 75 80
 Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
 85 90 95
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
 100 105 110
 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
 115 120 125
 Asn Asp Gly Val Leu Lys Val Thr Ile Pro Lys Leu Pro Pro Pro Glu
 130 135 140
 Pro Lys Lys Pro Lys Thr Ile Gln Val Gln Val Ala
 145 150 155

<210> 5
 <211> 1311
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (133)..(1083)

<400> 5
 cggcagcaggt ccacatgaaa ttcgattctc acatttcttc tatttaattc gaatttcaaa 60
 ttgccatttc tcgattccg gggaaagaaa aaaaaaacct agaaaagtgt tttctccgtt 120
 ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171
 Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
 1 5 10

ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat	219
Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
15 20 25	
aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
30 35 40 45	
cag gcg cag gaa gcc gga gct cgt ctc cac gct ttg atc tct tct aat	315
Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
50 55 60	
cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
80 85 90	
cgt gtg att ggt gtt cgc gaa gaa tgt cgg att agg gaa cag gat ttt	459
Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
95 100 105	
ggg aat ttt cag gtt aaa gag cga atg aga gca acg aaa aag gtc aga	507
Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
110 115 120 125	
gag aga ttt ggc cgc ttt ttt tac cgg ttc ccg gag gga gaa tcc gcc	555
Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
130 135 140	
gcc gat gtc ttc gat cgc gtc tcc agt ttt ctc gag tct cta tgg aga	603
Ala Asp Val Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg	
145 150 155	
gac att gac atg aac aga ctg cac atc aac ccg tct cat gag cta aac	651
Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
160 165 170	
ttt gtg att gtc tca cat ggc tta aca tcg cgt gtg ttt ctg atg aaa	699
Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
tgg ttt aag tgg tca gtg gaa cag ttc gag gga cta aac aat cca ggg	747
Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
190 195 200 205	
aac agt gag atc aga gtg atg gaa tta gga caa ggc ggt gat tac agc	795
Asn Ser Glu Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser	
210 215 220	
ttg gcg att cat cac aca gag gaa gag tta gcc aca tgg gga ctg tca	843
Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc	891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly
 240 245 250
 gaa tgg aaa gaa gat tgt aag tgg tat ttt ggt gat ttc ttc gac cat 939
 Glu Trp Lys Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His
 255 260 265
 atg gca gat tcc gat aaa gag tgc gag act gag gcc act gaa gat aga 987
 Met Ala Asp Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg
 270 275 280 285
 gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035
 Glu Glu Glu Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser
 290 295 300
 tca gaa tat agc aat gag cca gag tta tac aat gga caa tgc tgc tga 1083
 Ser Glu Tyr Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys
 305 310 315
 tactatttta cagaacaaaa gcatacatga gaagaaacgt ttaactaaag aattcagaag 1143
 atttgatttt gataaaaact tgtaccaatt tactgattaa gctttctggt gtcttagttt 1203
 gtagcttttg gtttgtggaa aagtgttgta cacatcgta taacaccagg aaacattaca 1263
 ggaaatttga aagattcatt ttattgtgac aaaaaaaaaa aaaaaaaaaa 1311

 <210> 6
 <211> 316
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 6
 Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile Leu Val Arg
 1 5 10 15
 His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr Thr Thr Thr
 20 25 30
 Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu Gln Ala Gln
 35 40 45
 Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser
 50 55 60
 Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp Arg Thr Arg
 65 70 75 80
 Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile
 85 90 95
 Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe Gly Asn Phe
 100 105 110
 Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe
 115 120 125

Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala Ala Asp Val
 130 135 140
 Phe Asp Arg Val Ser Ser Phe Leu Glu Ser Leu Trp Arg Asp Ile Asp
 145 150 155 160
 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile
 165 170 175
 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys
 180 185 190
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu
 195 200 205
 Ile Arg Val Met Glu Leu Gly Gln Gly Gly Asp Tyr Ser Leu Ala Ile
 210 215 220
 His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser Pro Glu Met
 225 230 235 240
 Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly Glu Trp Lys
 245 250 255
 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp
 260 265 270
 Ser Asp Lys Glu Cys Glu Thr Glu Ala Thr Glu Asp Arg Glu Glu Glu
 275 280 285
 Glu Glu Glu Glu Gly Lys Arg Val Asn Leu Leu Thr Ser Ser Glu Tyr
 290 295 300
 Ser Asn Glu Pro Glu Leu Tyr Asn Gly Gln Cys Cys
 305 310 315

<210> 7
 <211> 863
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (19) .. (837)

<400> 7
 agagacagta aacctaata atg gcg aac tca gac aaa aga tta ttc gag aag 51
 Met Ala Asn Ser Asp Lys Arg Leu Phe Glu Lys
 1 5 10
 gta gct ata ata acc gga gga gca aga ggg ata gga gcg gcc acg gcg 99
 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala
 15 20 25

aga ttg ttc aca gag aat ggc gcg tat gtg ata gtc gcg gat atc ctt	147
Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
30 35 40	
gat aat gaa ggc atc ctt gtg gcg gaa tcg atc ggt ggg tgt tac gtt	195
Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
45 50 55	
cat tgt gac gta tcg aag gag gct gat gtt gag gcg gca gtg gag cta	243
His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
60 65 70 75	
gca atg aga cgt aaa ggt aga cta gat gtg atg ttc aac aat gcc ggg	291
Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
tgc aca tcg agc tca tca ggg cta atg gga gga ctt gga gga cat gcg	483
Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
140 145 150 155	
tat acg ctc tcc aaa gga ggc atc aac ggg gtg gtg agg aca acg gag	531
Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
tgc gag ctt ggg tct cac ggc atc cgt gtg aat agc atc tct cct cat	579
Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
gga gtt ccc act gac atc ttg gtt aat gcg tac cgt aag ttc ctt aac	627
Gly Val Pro Thr Asp Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn	
190 195 200	
aat gac aaa ctc aac gtc gct gag gtc acc gac att att gct gag aaa	675
Asn Asp Lys Leu Asn Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys	
205 210 215	
ggg agt ttg ctg acc gga aga gcc ggt act gtg gag gac gta gct caa	723
Gly Ser Leu Leu Thr Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln	
220 225 230 235	
gca gct ttg ttt ctt gca agc caa gaa tcg tcg ggg ttc att acc gga	771
Ala Ala Leu Phe Leu Ala Ser Gln Glu Ser Ser Gly Phe Ile Thr Gly	
240 245 250	
cat aac ttg gtt gtt gat ggt ggt tac aca tct gcc act agt act atg	819

His Asn Leu Val Val Asp Gly Gly Tyr Thr Ser Ala Thr Ser Thr Met
 255 260 265

aga ttt atc tac aac tag ttttcgtttg gtggtgtttc cttttc
 Arg Phe Ile Tyr Asn
 270

863

<210> 8

<211> 272

<212> PRT

<213> Arabidopsis thaliana

<400> 8

Met Ala Asn Ser Asp Lys Arg Leu Phe Glu Lys Val Ala Ile Ile Thr
 1 5 10 15

Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala Arg Leu Phe Thr Glu
 20 25 30

Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu Asp Asn Glu Gly Ile
 35 40 45

Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val His Cys Asp Val Ser
 50 55 60

Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu Ala Met Arg Arg Lys
 65 70 75 80

Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly Met Ser Leu Asn Glu
 85 90 95

Gly Ser Ile Met Gly Met Asp Val Asp Met Val Asn Lys Leu Val Ser
 100 105 110

Val Asn Val Asn Gly Val Leu His Gly Ile Lys His Ala Ala Lys Ala
 115 120 125

Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile Cys Thr Ser Ser Ser
 130 135 140

Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys
 145 150 155 160

Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu Cys Glu Leu Gly Ser
 165 170 175

His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp
 180 185 190

Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn
 195 200 205

Val Ala Glu Val Thr Asp Ile Ile Ala Glu Lys Gly Ser Leu Leu Thr
 210 215 220

Gly Arg Ala Gly Thr Val Glu Asp Val Ala Gln Ala Ala Leu Phe Leu

225		230		235		240									
Ala	Ser	Gln	Glu	Ser	Ser	Gly	Phe	Ile	Thr	Gly	His	Asn	Leu	Val	Val
				245					250					255	
Asp	Gly	Gly	Tyr	Thr	Ser	Ala	Thr	Ser	Thr	Met	Arg	Phe	Ile	Tyr	Asn
			260					265						270	

<210> 9
 <211> 3107
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(34)

<220>
 <221> CDS
 <222> (958)..(1054)

<220>
 <221> CDS
 <222> (1209)..(1486)

<220>
 <221> CDS
 <222> (1578)..(2354)

<220>
 <221> CDS
 <222> (2440)..(2529)

<220>
 <221> CDS
 <222> (2629)..(2790)

<220>
 <221> CDS
 <222> (2884)..(2943)

<400> 9
 tcaaccttct atcatcacc atg gat cct tac aag gtatcttcga tcatattctt 54
 Met Asp Pro Tyr Lys
 1 5

cttacttttt ctttggtttt gtgtggtgta tgtgtatctt aattagaatt aggttcaact 114
 atatatgctc gttttctaaa ctatttttta attggattga tgttcttaaa tcttaagggt 174
 caaaatactt tttatgctca aaaacttact taaattctgt gatcgcttga acctaagtgg 234
 atgatgtgga tttcctggtt tggctgccta tctttaagta aaacgtttta cccactgcgt 294
 gagaaagaca cgccacatgt ggtttttggt gtttttttcc ttagattaga agttattttg 354

ttgttgTTTT tttttttata gtatgacaca catgtgttct aaaaatcgga cgttcaaAtg 414
 atataatcga ttgttttagac gtccgaccgt atattatttt agtgatatca gccaaatcag 474
 attaagtaat catcaacaaa atgattgac agatctatca atacaagtgt attttttttt 534
 cacatacaaa aaaattatct caccgacgaa aaaaaataa aaaattatta tgtagatcca 594
 tcgaacaaaa ggcttgaata tcggaagtca cttaaaagtG taataatcga ataaatatta 654
 gtggataaaa tgaaatttat ctacaaccct actctccgac atgttactgt ttgcgtcatc 714
 aaatctaaag cctttttggc aaataatggt cggaagacta ctcgtgtcgg gatggaccac 774
 ccggatccga tcaggaaacg ggttttgata tgtttcgggt tacgacaaaa aattagggct 834
 ttttatcaaa tcaatcagtt ggtagtaaaa ttttgTggat tgttcttgTc gattccgttt 894
 gattgttgac caaatttctt cctaggattt tgttgataat cgatcgtata atgggtgattg 954
 cag tat cgt cct tca agc gcg tac aac gcc cca ttc tac acc aca aac 1002
 Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro Phe Tyr Thr Thr Asn
 10 15 20
 ggt ggt gct cca gtc tcc aac aac atc tct tcc ctc acc atc gga gaa 1050
 Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser Leu Thr Ile Gly Glu
 25 30 35
 aga g gtatcgtaac cctgaatttc aagagtctat caataagaat cggaacttgt 1104
 Arg G
 tggatttatg aaagagataa aactgagata tagagtctaa gctgagatct gttcgtgaag 1164
 cgtgatgtga ttatttttaa catgtgttac ttcgtaatgg gcag gt ccg gtt ctt 1219
 ly Pro Val Leu
 40
 ctt gag gat tat cat ttg atc gag aag gtt gct aat ttc acc aga gag 1267
 Leu Glu Asp Tyr His Leu Ile Glu Lys Val Ala Asn Phe Thr Arg Glu
 45 50 55
 agg atc cct gag aga gtg gtt cat gct aga gga atc agt gct aag ggt 1315
 Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ile Ser Ala Lys Gly
 60 65 70
 ttc ttt gaa gtc acc cat gac att tca aac ctc act tgt gct gat ttt 1363
 Phe Phe Glu Val Thr His Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe
 75 80 85
 ctc aga gcc cct ggt gtt caa act ccg gtt att gtc cgt ttc tca acg 1411
 Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val Arg Phe Ser Thr
 90 95 100 105
 gtt gtt cac gga cgt gcc agt cct gaa acc atg agg gat att cgt ggt 1459
 Val Val His Gly Arg Ala Ser Pro Glu Thr Met Arg Asp Ile Arg Gly
 110 115 120

ttt gct gtc aag ttt tac acc aga gag gtataagaaa gattcaaagt 1506
 Phe Ala Val Lys Phe Tyr Thr Arg Glu
 125 130

ttccattttt aatcgtcttt tagcttcttt agaatcagga ctgatttttg tcttggtact 1566
 gttatgatca g gga aac ttt gat ctt gtt ggg aac aac act ccg gtg ttc 1616
 Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
 135 140

ttc atc cgt gat ggg att cag ttc ccg gat gtt gtc cac gcg ttg aaa 1664
 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
 145 150 155

cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac 1712
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
 160 165 170 175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat 1760
 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
 180 185 190

gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc 1808
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
 195 200 205

cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag 1856
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
 210 215 220

ttc cac tgg aaa cca act tgt ggg atc aag aat ctg act gat gaa gag 1904
 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu
 225 230 235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc 1952
 Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
 240 245 250 255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc 2000
 His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
 260 265 270

cag acc atg gat cct gca gat gag gat aag ttt gac ttt gac cca ctt 2048
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
 275 280 285

gat gtg acc aag atc tgg cct gag gat att ttg cct ctg caa ccg gtt 2096
 Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
 290 295 300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act 2144
 Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
 305 310 315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac 2192
 Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

320	325	330	335	
tca gac gac aag ctg ctc cag tgt agg atc ttt gct tat ggt gac act				2240
Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
cag aga cat cgc ctt gga ccg aat tat ttg cag ctt cca gtc aat gct				2288
Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc				2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
atg cac aga gat gag gag gtacgtctta gtacaccact tgagctacca				2384
Met His Arg Asp Glu Glu	385			
ttgttagtct ttttacttgg aatcaaaatt ctcatttggg ttgtactttt tacag atc				2442
			Ile	390
aat tac tac ccc tca aag ttt gat cct gtc cgc tgc gct gag aaa gtt				2490
Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
ccc acc cct aca aac tcc tac act gga att cga aca aag gtccgattcc				2539
Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
tgccatgcct tctctaaatc ttcaaactct aaactcaagt ttattagaat attggtgcta				2599
agaaaaacatt ttaattgcta atgttgacg tgc gtc atc aag aaa gag aac aac				2652
		Cys Val Ile Lys Lys Glu Asn Asn	425	
420				
ttc aaa cag gct gga gac agg tac aga tca tgg gca cca gac agg caa				2700
Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln	430	435	440	
gac agg ttt gtt aag aga tgg gtg gag att cta tgc gag cca cgt ctc				2748
Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
acc cac gag atc cgc ggc atc tgg acc tct tac tgg ctc aag				2790
Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
gtcagaacca aaaaaacact cgggtcaaatt tctacgtcct tttaccaag tttcagcaaa				2850
ctaaaacatt atttatctct ctgtatctct cag gct gat cga tcc ttg gga cag				2904
		Ala Asp Arg Ser Leu Gly Gln	480	
475				
aaa ctc gca agc cgt ctg aac gtg agg cca agc atc tag aggccaatct				2953
Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

ccatataagc tcagtctatg tgagggtacaa tcaatctcat cgatctatca tcgcttggtc 3013
 gttaaatccg tcaaaaagat aatcacatgt gttgttggtt cttgtctata taataataat 3073
 gcttgtaatc ccaaaaactc atgtttcctt cctt 3107

<210> 10
 <211> 492
 <212> PRT
 <213> Arabidopsis thaliana

<400> 10

Met Asp Pro Tyr Lys Tyr Arg Pro Ser Ser Ala Tyr Asn Ala Pro
 1 5 10 15
 Phe Tyr Thr Thr Asn Gly Gly Ala Pro Val Ser Asn Asn Ile Ser Ser
 20 25 30
 Leu Thr Ile Gly Glu Arg Gly Pro Val Leu Leu Glu Asp Tyr His Leu
 35 40 45
 Ile Glu Lys Val Ala Asn Phe Thr Arg Glu Arg Ile Pro Glu Arg Val
 50 55 60
 Val His Ala Arg Gly Ile Ser Ala Lys Gly Phe Phe Glu Val Thr His
 65 70 75 8
 Asp Ile Ser Asn Leu Thr Cys Ala Asp Phe Leu Arg Ala Pro Gly Val
 85 90 95
 Gln Thr Pro Val Ile Val Arg Phe Ser Thr Val Val His Gly Arg Ala
 100 105 110
 Ser Pro Glu Thr Met Arg Asp Ile Arg Gly Phe Ala Val Lys Phe Tyr
 115 120 125
 Thr Arg Glu Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
 130 135 140
 Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
 145 150 155 16
 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
 165 170 175
 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
 180 185 190
 Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
 195 200 205
 His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
 210 215 220
 Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu

225 230 235 24
 Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
 245 250 255
 His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
 260 265 270
 Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
 275 280 285
 Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
 290 295 300
 Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
 305 310 315 32
 Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr
 325 330 335
 Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr
 340 345 350
 Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala
 355 360 365
 Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe
 370 375 380
 Met His Arg Asp Glu Glu Ile Asn Tyr Tyr Pro Ser Lys Phe Asp Pro
 385 390 395 40
 Val Arg Cys Ala Glu Lys Val Pro Thr Pro Thr Asn Ser Tyr Thr Gly
 405 410 415
 Ile Arg Thr Lys Cys Val Ile Lys Lys Glu Asn Asn Phe Lys Gln Ala
 420 425 430
 Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln Asp Arg Phe Val
 435 440 445
 Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu Thr His Glu Ile
 450 455 460
 Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys Ala Asp Arg Ser Leu Gly
 465 470 475 48
 Gln Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile
 485 490

<210> 11

<211> 2687

<212> DNA

<213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (67)..(204)

<220>
 <221> CDS
 <222> (521)..(661)

<220>
 <221> CDS
 <222> (745)..(1026)

<220>
 <221> CDS
 <222> (1114)..(2667)

<400> 11
 aagttcctcaaa tttctctctta gcattctctt tcgtttctcg ttttcgttga atcaaagttc 60
 gttgcg atg gcg gat gtt cag atg gct gat gca gaa act ttt gct ttc 108
 Met Ala Asp Val Gln Met Ala Asp Ala Glu Thr Phe Ala Phe
 1 5 10
 caa gct gag att aac cag ctt ctt agc ttg atc atc aac acg ttc tac 156
 Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr
 15 20 25 30
 agc aac aaa gaa atc ttc ctc cgt gag ctc atc agt aac tct tct gat 204
 Ser Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp
 35 40 45
 gtaagtttcc cttcaaatct ctctctgact cgggtgtgact cgtccgcttc ctattttctt 264
 gactgttggt tgttctttta ttccctggatt cgttgatagc gttggattcg taggttttagc 324
 gttgtgattg cttattcaaa taaatcgtga tttggcttgt gcatcacgtt aagtttagaa 384
 ttcttagctt gtgctcgatc ttcatgtgtt gtagttacat atatagaacg gttcttgctt 444
 cgatgtagtt tttgatttac cctagaggat tgagtaaagc ttctgattat ctttgtttat 504
 atgaacggtt ttgtag gct ctt gac aag att cga ttt gag agc tta acg gat 556
 Ala Leu Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp
 50 55
 aag agc aag ctc gat gga cag cct gaa ctc ttc att aga ttg gtt cct 604
 Lys Ser Lys Leu Asp Gly Gln Pro Glu Leu Phe Ile Arg Leu Val Pro
 60 65 70
 gac aag cct aat aag acg ctc tca att att gac agt ggt att ggc atg 652
 Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
 75 80 85 90
 acc aaa gca ggtaacgaat caatgcctaa taatctctcg ttggtgagat 701
 Thr Lys Ala
 gtttagtgta tgtgctgtgg ttatgactct ctattatttt tca gat ttg gtg aac 756

Asp Leu Val Asn
95

aac ttg gga acc att gcg agg tct gga aca aaa gag ttt atg gag gcg 804
Asn Leu Gly Thr Ile Ala Arg Ser Gly Thr Lys Glu Phe Met Glu Ala
100 105 110

ctt caa gct gga gct gat gta agc atg ata gga caa ttt ggt gtt ggt 852
Leu Gln Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val Gly
115 120 125

ttc tac tct gct tat ctt gtt gca gag aag gtt gtt gtc act aca aag 900
Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val Val Thr Thr Lys
130 135 140 145

cac aat gat gat gaa caa tac gtt tgg gag tct caa gct ggt ggt tcc 948
His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly Ser
150 155 160

ttc act gtc act agg gat gtg gat ggg gaa cca ctt ggt aga gga act 996
Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly Thr
165 170 175

aag atc agc ctc ttc ctt aag gac gat cag gtaaggaatc gtagctttga 1046
Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln
180 185

gtgttttggg ggatgttctt ttcttttggg gttttctgtg ttcttacaag tgtgtttatt 1106

catgcag ctt gaa tac ttg gag gag agg aga ctc aaa gac ttg gtg aag 1155
Leu Glu Tyr Leu Glu Glu Arg Arg Leu Lys Asp Leu Val Lys
190 195 200

aag cac tct gag ttc atc agt tac cct atc tac ctt tgg acc gag aaa 1203
Lys His Ser Glu Phe Ile Ser Tyr Pro Ile Tyr Leu Trp Thr Glu Lys
205 210 215

acc acc gag aag gag atc agt gac gat gag gat gaa gat gaa cca aag 1251
Thr Thr Glu Lys Glu Ile Ser Asp Asp Glu Asp Glu Asp Glu Pro Lys
220 225 230

aaa gaa aac gaa ggt gag gtt gaa gaa gtt gat gag aag aag gag aaa 1299
Lys Glu Asn Glu Gly Glu Val Glu Glu Val Asp Glu Lys Lys Glu Lys
235 240 245

gat ggt aaa aag aag aag aaa atc aag gaa gtc tct cac gag tgg gaa 1347
Asp Gly Lys Lys Lys Lys Lys Ile Lys Glu Val Ser His Glu Trp Glu
250 255 260 265

ctc atc aac aag cag aaa ccg atc tgg ttg agg aag cca gaa gag atc 1395
Leu Ile Asn Lys Gln Lys Pro Ile Trp Leu Arg Lys Pro Glu Glu Ile
270 275 280

act aag gaa gag tat gct gct ttc tac aag agc ttg acc aat gac tgg 1443
Thr Lys Glu Glu Tyr Ala Ala Phe Tyr Lys Ser Leu Thr Asn Asp Trp
285 290 295

gaa gat cac tta gcc gtg aaa cac ttc tca gtg gag ggt cag cta gaa	1491
Glu Asp His Leu Ala Val Lys His Phe Ser Val Glu Gly Gln Leu Glu	
300 305 310	
ttc aag gcc att ctc ttt gta cca aag aga gct ccg ttt gat ctc ttt	1539
Phe Lys Ala Ile Leu Phe Val Pro Lys Arg Ala Pro Phe Asp Leu Phe	
315 320 325	
gac acg agg aag aag ttg aat aac atc aag ctt tat gtc agg agg gtg	1587
Asp Thr Arg Lys Lys Leu Asn Asn Ile Lys Leu Tyr Val Arg Arg Val	
330 335 340 345	
ttc att atg gac aac tgt gaa gag cta atc cca gag tac ctc agc ttt	1635
Phe Ile Met Asp Asn Cys Glu Glu Leu Ile Pro Glu Tyr Leu Ser Phe	
350 355 360	
gtg aaa ggt gtt gtt gac tct gat gac ttg cca ctc aac atc tct cgt	1683
Val Lys Gly Val Val Asp Ser Asp Leu Pro Leu Asn Ile Ser Arg	
365 370 375	
gag acg ctt caa cag aac aag atc ctt aag gtg atc agg aag aat cta	1731
Glu Thr Leu Gln Gln Asn Lys Ile Leu Lys Val Ile Arg Lys Asn Leu	
380 385 390	
gtg aag aag tgc att gag atg ttc aac gag att gct gag aac aaa gag	1779
Val Lys Lys Cys Ile Glu Met Phe Asn Glu Ile Ala Glu Asn Lys Glu	
395 400 405	
gac tac acc aaa ttc tat gag gct ttc tcc aag aat ctc aaa ttg ggt	1827
Asp Tyr Thr Lys Phe Tyr Glu Ala Phe Ser Lys Asn Leu Lys Leu Gly	
410 415 420 425	
atc cat gaa gac agt cag aac agg gga aag att gct gat ctt cta cgg	1875
Ile His Glu Asp Ser Gln Asn Arg Gly Lys Ile Ala Asp Leu Leu Arg	
430 435 440	
tac cac tcc aca aag agt ggt gat gaa atg acg agc ttc aaa gat tac	1923
Tyr His Ser Thr Lys Ser Gly Asp Glu Met Thr Ser Phe Lys Asp Tyr	
445 450 455	
gtc aca agg atg aag gaa ggt caa aag gac att ttc tac atc act ggt	1971
Val Thr Arg Met Lys Glu Gly Gln Lys Asp Ile Phe Tyr Ile Thr Gly	
460 465 470	
gaa agc aaa aag gcg gtg gag aat tcc ttc ttg gag agg ctg aag aag	2019
Glu Ser Lys Lys Ala Val Glu Asn Ser Phe Leu Glu Arg Leu Lys Lys	
475 480 485	
aga ggc tac gag gta ctt tac atg gtg gat gcg att gac gaa tac gct	2067
Arg Gly Tyr Glu Val Leu Tyr Met Val Asp Ala Ile Asp Glu Tyr Ala	
490 495 500 505	
gtt gga caa ttg aag gag tat gac ggt aag aaa ctt gtt tct gcg act	2115
Val Gly Gln Leu Lys Glu Tyr Asp Gly Lys Lys Leu Val Ser Ala Thr	
510 515 520	
aaa gaa ggc ctc aaa ctt gaa gat gag acc gaa gaa gag aag aaa aag	2163

Lys Glu Gly Leu Lys Leu Glu Asp Glu Thr Glu Glu Glu Lys Lys Lys
 525 530 535
 agg gaa gag aag aag aag tcc ttc gag aat ctc tgc aag acg att aag 2211
 Arg Glu Glu Lys Lys Lys Ser Phe Glu Asn Leu Cys Lys Thr Ile Lys
 540 545 550
 gaa att ctc ggg gac aag gtt gag aag gtt gtg gtc tca gac agg att 2259
 Glu Ile Leu Gly Asp Lys Val Glu Lys Val Val Val Ser Asp Arg Ile
 555 560 565
 gtg gac tct ccc tgc tgt cta gta act ggt gaa tat gga tgg act gca 2307
 Val Asp Ser Pro Cys Cys Leu Val Thr Gly Glu Tyr Gly Trp Thr Ala
 570 575 580 585
 aat atg gag agg att atg aag gca cag gcc ttg aga gat agc agc atg 2355
 Asn Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Ser Ser Met
 590 595 600
 agt ggt tac atg tcg agc aag aaa aca atg gag atc aac ccc gac aac 2403
 Ser Gly Tyr Met Ser Ser Lys Lys Thr Met Glu Ile Asn Pro Asp Asn
 605 610 615
 ggt ata atg gag gac ctc agg aag aga gct gaa gca gac aag aat gac 2451
 Gly Ile Met Glu Asp Leu Arg Lys Arg Ala Glu Ala Asp Lys Asn Asp
 620 625 630
 aag tct gtt aaa gat ctt gtc atg ttg ctg tat gag aca gct ttg ttg 2499
 Lys Ser Val Lys Asp Leu Val Met Leu Leu Tyr Glu Thr Ala Leu Leu
 635 640 645
 acg tct gga ttt agt ctt gat gaa ccg aac act ttt gct gct agg att 2547
 Thr Ser Gly Phe Ser Leu Asp Glu Pro Asn Thr Phe Ala Ala Arg Ile
 650 655 660 665
 cac agg atg ttg aag ttg ggt ctg agt att gat gag gat gag aac gtt 2595
 His Arg Met Leu Lys Leu Gly Leu Ser Ile Asp Glu Asp Glu Asn Val
 670 675 680
 gag gaa gat ggt gat atg cct gag ttg gag gag gac gct gct gaa gag 2643
 Glu Glu Asp Gly Asp Met Pro Glu Leu Glu Glu Asp Ala Ala Glu Glu
 685 690 695
 agc aag atg gag gaa gtc gac taa gagatgaaga aattgctctt 2687
 Ser Lys Met Glu Glu Val Asp 705
 700

<210> 12

<211> 704

<212> PRT

<213> Arabidopsis thaliana

<400> 12

Met Ala Asp Val Gln Met Ala Asp Ala Glu Thr Phe Ala Phe Gln Ala
 1 5 10 15

Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn
 20 25 30
 Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
 35 40 45
 Asp Lys Ile Arg Phe Glu Ser Leu Thr Asp Lys Ser Lys Leu Asp Gly
 50 55 60
 Gln Pro Glu Leu Phe Ile Arg Leu Val Pro Asp Lys Pro Asn Lys Thr
 65 70 75 80
 Leu Ser Ile Ile Asp Ser Gly Ile Gly Met Thr Lys Ala Asp Leu Val
 85 90 95
 Asn Asn Leu Gly Thr Ile Ala Arg Ser Gly Thr Lys Glu Phe Met Glu
 100 105 110
 Ala Leu Gln Ala Gly Ala Asp Val Ser Met Ile Gly Gln Phe Gly Val
 115 120 125
 Gly Phe Tyr Ser Ala Tyr Leu Val Ala Glu Lys Val Val Val Thr Thr
 130 135 140
 Lys His Asn Asp Asp Glu Gln Tyr Val Trp Glu Ser Gln Ala Gly Gly
 145 150 155 160
 Ser Phe Thr Val Thr Arg Asp Val Asp Gly Glu Pro Leu Gly Arg Gly
 165 170 175
 Thr Lys Ile Ser Leu Phe Leu Lys Asp Asp Gln Leu Glu Tyr Leu Glu
 180 185 190
 Glu Arg Arg Leu Lys Asp Leu Val Lys Lys His Ser Glu Phe Ile Ser
 195 200 205
 Tyr Pro Ile Tyr Leu Trp Thr Glu Lys Thr Thr Glu Lys Glu Ile Ser
 210 215 220
 Asp Asp Glu Asp Glu Asp Glu Pro Lys Lys Glu Asn Glu Gly Glu Val
 225 230 235 240
 Glu Glu Val Asp Glu Lys Lys Glu Lys Asp Gly Lys Lys Lys Lys Lys
 245 250 255
 Ile Lys Glu Val Ser His Glu Trp Glu Leu Ile Asn Lys Gln Lys Pro
 260 265 270
 Ile Trp Leu Arg Lys Pro Glu Glu Ile Thr Lys Glu Glu Tyr Ala Ala
 275 280 285
 Phe Tyr Lys Ser Leu Thr Asn Asp Trp Glu Asp His Leu Ala Val Lys
 290 295 300
 His Phe Ser Val Glu Gly Gln Leu Glu Phe Lys Ala Ile Leu Phe Val
 305 310 315 320

Pro Lys Arg Ala Pro Phe Asp Leu Phe Asp Thr Arg Lys Lys Leu Asn
 325 330 335
 Asn Ile Lys Leu Tyr Val Arg Arg Val Phe Ile Met Asp Asn Cys Glu
 340 345 350
 Glu Leu Ile Pro Glu Tyr Leu Ser Phe Val Lys Gly Val Val Asp Ser
 355 360 365
 Asp Asp Leu Pro Leu Asn Ile Ser Arg Glu Thr Leu Gln Gln Asn Lys
 370 375 380
 Ile Leu Lys Val Ile Arg Lys Asn Leu Val Lys Lys Cys Ile Glu Met
 385 390 395 400
 Phe Asn Glu Ile Ala Glu Asn Lys Glu Asp Tyr Thr Lys Phe Tyr Glu
 405 410 415
 Ala Phe Ser Lys Asn Leu Lys Leu Gly Ile His Glu Asp Ser Gln Asn
 420 425 430
 Arg Gly Lys Ile Ala Asp Leu Leu Arg Tyr His Ser Thr Lys Ser Gly
 435 440 445
 Asp Glu Met Thr Ser Phe Lys Asp Tyr Val Thr Arg Met Lys Glu Gly
 450 455 460
 Gln Lys Asp Ile Phe Tyr Ile Thr Gly Glu Ser Lys Lys Ala Val Glu
 465 470 475 480
 Asn Ser Phe Leu Glu Arg Leu Lys Lys Arg Gly Tyr Glu Val Leu Tyr
 485 490 495
 Met Val Asp Ala Ile Asp Glu Tyr Ala Val Gly Gln Leu Lys Glu Tyr
 500 505 510
 Asp Gly Lys Lys Leu Val Ser Ala Thr Lys Glu Gly Leu Lys Leu Glu
 515 520 525
 Asp Glu Thr Glu Glu Glu Lys Lys Lys Arg Glu Glu Lys Lys Lys Ser
 530 535 540
 Phe Glu Asn Leu Cys Lys Thr Ile Lys Glu Ile Leu Gly Asp Lys Val
 545 550 555 560
 Glu Lys Val Val Val Ser Asp Arg Ile Val Asp Ser Pro Cys Cys Leu
 565 570 575
 Val Thr Gly Glu Tyr Gly Trp Thr Ala Asn Met Glu Arg Ile Met Lys
 580 585 590
 Ala Gln Ala Leu Arg Asp Ser Ser Met Ser Gly Tyr Met Ser Ser Lys
 595 600 605
 Lys Thr Met Glu Ile Asn Pro Asp Asn Gly Ile Met Glu Asp Leu Arg
 610 615 620

Lys Arg Ala Glu Ala Asp Lys Asn Asp Lys Ser Val Lys Asp Leu Val
 625 630 635 640
 Met Leu Leu Tyr Glu Thr Ala Leu Leu Thr Ser Gly Phe Ser Leu Asp
 645 650 655
 Glu Pro Asn Thr Phe Ala Ala Arg Ile His Arg Met Leu Lys Leu Gly
 660 665 670
 Leu Ser Ile Asp Glu Asp Glu Asn Val Glu Glu Asp Gly Asp Met Pro
 675 680 685
 Glu Leu Glu Glu Asp Ala Ala Glu Glu Ser Lys Met Glu Glu Val Asp
 690 695 700

<210> 13
 <211> 2932
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(2924)

<400> 13
 ttgattgata ggcgata atg gcg ggt cgg aac ata gag aag atg gca tct 50
 Met Ala Gly Arg Asn Ile Glu Lys Met Ala Ser
 1 5 10
 att gat gct cag ctt cgg caa ctc gtt cct gct aaa gtc agt gaa gac 98
 Ile Asp Ala Gln Leu Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp
 15 20 25
 gat aag ctt gtt gag tac gat gct ctt ctc ctt gat cgc ttt ctc gac 146
 Asp Lys Leu Val Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp
 30 35 40
 att ctc cag gat tta cac ggc gag gat ctc cgt gaa acg gtt caa gag 194
 Ile Leu Gln Asp Leu His Gly Glu Asp Leu Arg Glu Thr Val Gln Glu
 45 50 55
 tta tac gag ctt tct gct gag tat gaa ggg aag cgt gag cct agc aag 242
 Leu Tyr Glu Leu Ser Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys
 60 65 70 75
 ctt gag gag cta ggg agt gtc cta acg agt ttg gat cct ggt gac tca 290
 Leu Glu Glu Leu Gly Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser
 80 85 90
 att gtt atc tcc aag gct ttc tct cac atg ctt aac tta gcc aat ttg 338
 Ile Val Ile Ser Lys Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu
 95 100 105
 gct gag gag gtg cag att gct cac cgt cgc agg atc aag aag ctg aag 386
 Ala Glu Glu Val Gln Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys

110	115	120	
aaa ggt gat ttc gtt gat gag agt tct gca act act gaa tcc gat att Lys Gly Asp Phe Val Asp Glu Ser Ser Ala Thr Thr Glu Ser Asp Ile 125 130 135			434
gaa gag act ttt aag agg ctc gtt tcg gat ctt ggt aag tct cct gaa Glu Glu Thr Phe Lys Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu 140 145 150 155			482
gag atc ttt gat gcc ttg aag aat cag act gtg gat ctg gtt ttg act Glu Ile Phe Asp Ala Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr 160 165 170			530
gct cat cct act cag tct gtg cgt aga tca ttg ctt cag aag cat ggg Ala His Pro Thr Gln Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly 175 180 185			578
agg ata agg gac tgt ctt gct caa ctc tat gca aag gac att act cct Arg Ile Arg Asp Cys Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro 190 195 200			626
gat gac aag cag gag cta gat gag tct ctg caa aga gag att caa gct Asp Asp Lys Gln Glu Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala 205 210 215			674
gca ttc cga aca gat gag att aga aga aca cct cca acc cca caa gat Ala Phe Arg Thr Asp Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp 220 225 230 235			722
gaa atg aga gct gga atg agt tat ttc cac gag aca atc tgg aaa ggt Glu Met Arg Ala Gly Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly 240 245 250			770
gtc ccc aag ttc ttg cgc cgt gtg gac aca gct ctg aaa aac att ggg Val Pro Lys Phe Leu Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly 255 260 265			818
att gat gaa cgt gtt cct tac aat gcc cca ttg att caa ttc tct tcg Ile Asp Glu Arg Val Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser 270 275 280			866
tgg atg ggc ggt gat cgt gat ggt aat ccg agg gtc aca cct gag gtc Trp Met Gly Gly Asp Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val 285 290 295			914
act aga gat gtg tgc ttg ttg gct aga atg atg gct gcc aat ctc tac Thr Arg Asp Val Cys Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr 300 305 310 315			962
tat aac caa atc gag aat ctg atg ttt gag tta tct atg tgg cgt tgc Tyr Asn Gln Ile Glu Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys 320 325 330			1010
act gat gaa ttc cgt gtg cgg gcg gat gaa ctg cac agg aac tca agg Thr Asp Glu Phe Arg Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg 335 340 345			1058

aaa gat gct gca aaa cat tac ata gaa ttc tgg aag aca att cct cca	1106
Lys Asp Ala Ala Lys His Tyr Ile Glu Phe Trp Lys Thr Ile Pro Pro	
350 355 360	
act gag cca tac cgt gtg att ctt ggt gat gtg agg gat aag ctg tat	1154
Thr Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr	
365 370 375	
cac aca cgt gag cgt tcc cgc caa ttg ctg agt aat gga atc tcg gat	1202
His Thr Arg Glu Arg Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp	
380 385 390 395	
att cct gaa gaa gct acc ttc act aat gtg gaa cag ttc ttg gag cct	1250
Ile Pro Glu Glu Ala Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro	
400 405 410	
ctt gag ctc tgt tac cga tca cta tgt tca tgt ggt gac agc ccg ata	1298
Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile	
415 420 425	
gct gat gga agc ctt ctt gat ttc ttg agg caa gtc tct acc ttt gga	1346
Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly	
430 435 440	
ctc tcc ctt gtg aga ctt gac atc agg caa gag tct gaa cgc cac aca	1394
Leu Ser Leu Val Arg Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr	
445 450 455	
gat gtc ttg gat gct atc acc aag cac ttg gac atc ggt tcc tcc tat	1442
Asp Val Leu Asp Ala Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr	
460 465 470 475	
aga gac tgg tct gaa gaa ggc cga cag gaa tgg ctt ctt gct gaa cta	1490
Arg Asp Trp Ser Glu Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu	
480 485 490	
agc ggc aaa cgt cca ctt ttc gga cct gat ctt ccc aaa acc gaa gaa	1538
Ser Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu	
495 500 505	
att tct gat gtc ctg gac aca ttc aaa gtc ata tct gag ctg cct tca	1586
Ile Ser Asp Val Leu Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser	
510 515 520	
gat tgt ttt gga gct tat att atc tct atg gca act tca cct agt gat	1634
Asp Cys Phe Gly Ala Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp	
525 530 535	
gtg ctt gcg gtt gag ctt tta cag cgc gaa tgc cat gtg aaa aat cca	1682
Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro	
540 545 550 555	
ctt aga gtt gtt cca ctc ttt gag aag cta gct gat ctt gaa gca gct	1730
Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala	
560 565 570	

cct gcc gct gtt gca aga ctc ttt tct ata gac tgg tac aaa aac cgt	1778
Pro Ala Ala Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg	
575 580 585	
att aac ggt aaa caa gag gtt atg att ggt tac tca gat tca ggg aaa	1826
Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys	
590 595 600	
gat gca ggg cgt ctc tca gct gct tgg gag cta tac aaa gct caa gaa	1874
Asp Ala Gly Arg Leu Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu	
605 610 615	
gag ctt gtg aag gtt gct aag aaa tat gga gtg aag cta act atg ttc	1922
Glu Leu Val Lys Val Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe	
620 625 630 635	
cat ggc cgt ggt ggc aca gtc gga aga gga ggt ggt cct act cat ctt	1970
His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu	
640 645 650	
gct ata ttg tct cag cca cca gat aca gtt aat ggc tct ctt cga gtc	2018
Ala Ile Leu Ser Gln Pro Pro Asp Thr Val Asn Gly Ser Leu Arg Val	
655 660 665	
acg gtt cag ggt gaa gtc att gag caa tca ttt ggg gag gca cac tta	2066
Thr Val Gln Gly Glu Val Ile Glu Gln Ser Phe Gly Glu Ala His Leu	
670 675 680	
tgc ttt aga aca ctt caa cgt ttc aca gca gct act cta gag cac gga	2114
Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His Gly	
685 690 695	
atg aac cct ccg att tca cca aaa ccc gag tgg cgt gct ttg ctt gat	2162
Met Asn Pro Pro Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp	
700 705 710 715	
gaa atg gcg gtt gtt gca act gag gaa tac cga tct gtc gtt ttc caa	2210
Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg Ser Val Val Phe Gln	
720 725 730	
gaa cct cga ttc gtc gag tat ttc cgc ctc gct act ccg gag ctg gag	2258
Glu Pro Arg Phe Val Glu Tyr Phe Arg Leu Ala Thr Pro Glu Leu Glu	
735 740 745	
tat gga cgt atg aat att gga agt aga cct tca aag cga aaa cca agc	2306
Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro Ser	
750 755 760	
ggt ggg atc gaa tct ctc cgt gca atc cca tgg atc ttt gct tgg acg	2354
Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr	
765 770 775	
caa aca aga ttc cat ctt cct gta tgg tta ggt ttc gga gca gca ttt	2402
Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala Phe	
780 785 790 795	
agg tat gcg atc aag aag gat gtg aga aac ctt cac atg ctg caa gat	2450

Arg Tyr Ala Ile Lys Lys Asp Val Arg Asn Leu His Met Leu Gln Asp
 800 805 810
 atg tat aaa caa tgg ccc ttt ttc cga gtc acc atc gat cta att gaa 2498
 Met Tyr Lys Gln Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Ile Glu
 815 820 825
 atg gtg ttc gcc aag gga gac ccc ggg atc gct gct ttg tac gac aaa 2546
 Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys
 830 835 840
 ctt ctt gtc tca gaa gat tta tgg gct ttt gga gag aaa ctc aga gcc 2594
 Leu Leu Val Ser Glu Asp Leu Trp Ala Phe Gly Glu Lys Leu Arg Ala
 845 850 855
 aac ttt gat gaa acc aag aac ctc gtc ctc cag act gct gga cat aaa 2642
 Asn Phe Asp Glu Thr Lys Asn Leu Val Leu Gln Thr Ala Gly His Lys
 860 865 870 875
 gac ctt ctt gaa gga gat cct tac ttg aaa cag aga cta agg cta cgt 2690
 Asp Leu Leu Glu Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg
 880 885 890
 gac tct tac att acg acc ctc aac gtt tgc caa gcc tac aca ttg aag 2738
 Asp Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Tyr Thr Leu Lys
 895 900 905
 agg atc cgt gat gca aac tac aat gtg act ctg cga cca cac att tct 2786
 Arg Ile Arg Asp Ala Asn Tyr Asn Val Thr Leu Arg Pro His Ile Ser
 910 915 920
 aaa gag atc atg caa tca agc aaa tca gca caa gag ctc gtc aag ctt 2834
 Lys Glu Ile Met Gln Ser Ser Lys Ser Ala Gln Glu Leu Val Lys Leu
 925 930 935
 aac ccc acg agt gaa tac gcg cct gga ctt gag gac aca ctt atc tta 2882
 Asn Pro Thr Ser Glu Tyr Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu
 940 945 950 955
 acc atg aag ggt att gct gca gga ttg caa aac acc ggt taa gtgagtca 2932
 Thr Met Lys Gly Ile Ala Ala Gly Leu Gln Asn Thr Gly
 960 965

<210> 14

<211> 968

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ala Gly Arg Asn Ile Glu Lys Met Ala Ser Ile Asp Ala Gln Leu
 1 5 10 15

Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp Asp Lys Leu Val Glu
 20 25 30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu

35	40	45
His Gly Glu Asp Leu Arg Glu Thr Val Gln Glu Leu Tyr Glu Leu Ser		
50	55	60
Ala Glu Tyr Glu Gly Lys Arg Glu Pro Ser Lys Leu Glu Glu Leu Gly		
65	70	75
Ser Val Leu Thr Ser Leu Asp Pro Gly Asp Ser Ile Val Ile Ser Lys		
85	90	95
Ala Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln		
100	105	110
Ile Ala His Arg Arg Arg Ile Lys Lys Leu Lys Lys Gly Asp Phe Val		
115	120	125
Asp Glu Ser Ser Ala Thr Thr Glu Ser Asp Ile Glu Glu Thr Phe Lys		
130	135	140
Arg Leu Val Ser Asp Leu Gly Lys Ser Pro Glu Glu Ile Phe Asp Ala		
145	150	155
Leu Lys Asn Gln Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln		
165	170	175
Ser Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Ile Arg Asp Cys		
180	185	190
Leu Ala Gln Leu Tyr Ala Lys Asp Ile Thr Pro Asp Asp Lys Gln Glu		
195	200	205
Leu Asp Glu Ser Leu Gln Arg Glu Ile Gln Ala Ala Phe Arg Thr Asp		
210	215	220
Glu Ile Arg Arg Thr Pro Pro Thr Pro Gln Asp Glu Met Arg Ala Gly		
225	230	235
Met Ser Tyr Phe His Glu Thr Ile Trp Lys Gly Val Pro Lys Phe Leu		
245	250	255
Arg Arg Val Asp Thr Ala Leu Lys Asn Ile Gly Ile Asp Glu Arg Val		
260	265	270
Pro Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser Trp Met Gly Gly Asp		
275	280	285
Arg Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys		
290	295	300
Leu Leu Ala Arg Met Met Ala Ala Asn Leu Tyr Tyr Asn Gln Ile Glu		
305	310	315
Asn Leu Met Phe Glu Leu Ser Met Trp Arg Cys Thr Asp Glu Phe Arg		
325	330	335
Val Arg Ala Asp Glu Leu His Arg Asn Ser Arg Lys Asp Ala Ala Lys		

340	345	350
His Tyr Ile Glu Phe Trp Lys Thr Ile Pro Pro Thr Glu Pro Tyr Arg 355 360 365		
Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr His Thr Arg Glu Arg 370 375 380		
Ser Arg Gln Leu Leu Ser Asn Gly Ile Ser Asp Ile Pro Glu Glu Ala 385 390 395 400		
Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro Leu Glu Leu Cys Tyr 405 410 415		
Arg Ser Leu Cys Ser Cys Gly Asp Ser Pro Ile Ala Asp Gly Ser Leu 420 425 430		
Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg 435 440 445		
Leu Asp Ile Arg Gln Glu Ser Glu Arg His Thr Asp Val Leu Asp Ala 450 455 460		
Ile Thr Lys His Leu Asp Ile Gly Ser Ser Tyr Arg Asp Trp Ser Glu 465 470 475 480		
Glu Gly Arg Gln Glu Trp Leu Leu Ala Glu Leu Ser Gly Lys Arg Pro 485 490 495		
Leu Phe Gly Pro Asp Leu Pro Lys Thr Glu Glu Ile Ser Asp Val Leu 500 505 510		
Asp Thr Phe Lys Val Ile Ser Glu Leu Pro Ser Asp Cys Phe Gly Ala 515 520 525		
Tyr Ile Ile Ser Met Ala Thr Ser Pro Ser Asp Val Leu Ala Val Glu 530 535 540		
Leu Leu Gln Arg Glu Cys His Val Lys Asn Pro Leu Arg Val Val Pro 545 550 555 560		
Leu Phe Glu Lys Leu Ala Asp Leu Glu Ala Ala Pro Ala Ala Val Ala 565 570 575		
Arg Leu Phe Ser Ile Asp Trp Tyr Lys Asn Arg Ile Asn Gly Lys Gln 580 585 590		
Glu Val Met Ile Gly Tyr Ser Asp Ser Gly Lys Asp Ala Gly Arg Leu 595 600 605		
Ser Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu Glu Leu Val Lys Val 610 615 620		
Ala Lys Lys Tyr Gly Val Lys Leu Thr Met Phe His Gly Arg Gly Gly 625 630 635 640		
Thr Val Gly Arg Gly Gly Gly Pro Thr His Leu Ala Ile Leu Ser Gln		

645										650					655				
Pro	Pro	Asp	Thr	Val	Asn	Gly	Ser	Leu	Arg	Val	Thr	Val	Gln	Gly	Glu				
			660					665					670						
Val	Ile	Glu	Gln	Ser	Phe	Gly	Glu	Ala	His	Leu	Cys	Phe	Arg	Thr	Leu				
		675					680					685							
Gln	Arg	Phe	Thr	Ala	Ala	Thr	Leu	Glu	His	Gly	Met	Asn	Pro	Pro	Ile				
	690					695					700								
Ser	Pro	Lys	Pro	Glu	Trp	Arg	Ala	Leu	Leu	Asp	Glu	Met	Ala	Val	Val				
	705				710					715					720				
Ala	Thr	Glu	Glu	Tyr	Arg	Ser	Val	Val	Phe	Gln	Glu	Pro	Arg	Phe	Val				
				725					730					735					
Glu	Tyr	Phe	Arg	Leu	Ala	Thr	Pro	Glu	Leu	Glu	Tyr	Gly	Arg	Met	Asn				
			740					745					750						
Ile	Gly	Ser	Arg	Pro	Ser	Lys	Arg	Lys	Pro	Ser	Gly	Gly	Ile	Glu	Ser				
		755					760					765							
Leu	Arg	Ala	Ile	Pro	Trp	Ile	Phe	Ala	Trp	Thr	Gln	Thr	Arg	Phe	His				
	770					775					780								
Leu	Pro	Val	Trp	Leu	Gly	Phe	Gly	Ala	Ala	Phe	Arg	Tyr	Ala	Ile	Lys				
	785				790					795					800				
Lys	Asp	Val	Arg	Asn	Leu	His	Met	Leu	Gln	Asp	Met	Tyr	Lys	Gln	Trp				
				805					810					815					
Pro	Phe	Phe	Arg	Val	Thr	Ile	Asp	Leu	Ile	Glu	Met	Val	Phe	Ala	Lys				
			820					825					830						
Gly	Asp	Pro	Gly	Ile	Ala	Ala	Leu	Tyr	Asp	Lys	Leu	Leu	Val	Ser	Glu				
		835					840					845							
Asp	Leu	Trp	Ala	Phe	Gly	Glu	Lys	Leu	Arg	Ala	Asn	Phe	Asp	Glu	Thr				
	850					855					860								
Lys	Asn	Leu	Val	Leu	Gln	Thr	Ala	Gly	His	Lys	Asp	Leu	Leu	Glu	Gly				
	865				870					875				880					
Asp	Pro	Tyr	Leu	Lys	Gln	Arg	Leu	Arg	Leu	Arg	Asp	Ser	Tyr	Ile	Thr				
				885				890						895					
Thr	Leu	Asn	Val	Cys	Gln	Ala	Tyr	Thr	Leu	Lys	Arg	Ile	Arg	Asp	Ala				
			900					905					910						
Asn	Tyr	Asn	Val	Thr	Leu	Arg	Pro	His	Ile	Ser	Lys	Glu	Ile	Met	Gln				
		915					920					925							
Ser	Ser	Lys	Ser	Ala	Gln	Glu	Leu	Val	Lys	Leu	Asn	Pro	Thr	Ser	Glu				
	930					935					940								
Tyr	Ala	Pro	Gly	Leu	Glu	Asp	Thr	Leu	Ile	Leu	Thr	Met	Lys	Gly	Ile				

945

950

955

960

Ala Ala Gly Leu Gln Asn Thr Gly
965

<210> 15

<211> 271

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (17) .. (259)

<400> 15

tcgattcagg ttaagg atg tgc aga gct aca tac att atc ggt gcc ctt gcg 52
Met Ser Arg Ala Thr Tyr Ile Ile Gly Ala Leu Ala
1 5 10

gga tct gcg gta gta gct tac gtg tgt gac aaa gtt att tct gat gat 100
Gly Ser Ala Val Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp
15 20 25

aag ctt ttt gga ggt act aca cca gga act att act aac aag gaa tgg 148
Lys Leu Phe Gly Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp
30 35 40

ggt gct gcg act gaa gag aga tta caa gca tgg cca aga gtt gct ggt 196
Gly Ala Ala Thr Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly
45 50 55 60

cct ccc gtc gtc atg aac cct atc agt cgc cag aat ttc atc gtc aag 244
Pro Pro Val Val Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys
65 70 75

tca cgt cct gaa taa cttttgatgc ct 271
Ser Arg Pro Glu
80

<210> 16

<211> 80

<212> PRT

<213> Arabidopsis thaliana

<400> 16

Met Ser Arg Ala Thr Tyr Ile Ile Gly Ala Leu Ala Gly Ser Ala Val
1 5 10 15

Val Ala Tyr Val Cys Asp Lys Val Ile Ser Asp Asp Lys Leu Phe Gly
20 25 30

Gly Thr Thr Pro Gly Thr Ile Thr Asn Lys Glu Trp Gly Ala Ala Thr
35 40 45

Glu Glu Arg Leu Gln Ala Trp Pro Arg Val Ala Gly Pro Pro Val Val
 50 55 60

Met Asn Pro Ile Ser Arg Gln Asn Phe Ile Val Lys Ser Arg Pro Glu
 65 70 75 80

<210> 17
 <211> 2580
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (30)..(143)

<220>
 <221> CDS
 <222> (295)..(417)

<220>
 <221> CDS
 <222> (582)..(632)

<220>
 <221> CDS
 <222> (1179)..(1245)

<220>
 <221> CDS
 <222> (1334)..(1383)

<220>
 <221> CDS
 <222> (1497)..(1577)

<220>
 <221> CDS
 <222> (1661)..(1740)

<220>
 <221> CDS
 <222> (1882)..(1984)

<220>
 <221> CDS
 <222> (2370)..(2564)

<400> 17
 tcttcacaaa tcctaaacga gtaggagct atg gct gca ccg att gtt gat gcg 53
 Met Ala Ala Pro Ile Val Asp Ala
 1 5

gag tac ttg aaa gag atc act aag gct cgc cgt gag ctc cgt tct ctc 101
 Glu Tyr Leu Lys Glu Ile Thr Lys Ala Arg Arg Glu Leu Arg Ser Leu
 10 15 20

atc gcg aac aag aac tgt gct cct atc atg ctc cga ttg gcg 143
 Ile Ala Asn Lys Asn Cys Ala Pro Ile Met Leu Arg Leu Ala
 25 30 35
 taagttttcg atttccttgg tttttcgtcg agttgactgt tacagatttc gtttattcat 203
 gtggagatcg ttcgattgta gttaggctgt agaatcgatt ttgtttgttt ttgaatgttg 263
 aaatgtttgt atcatctggg ttttatgaag a tgg cac gat gct gga acc tat 315
 Trp His Asp Ala Gly Thr Tyr
 40 45
 gat gct caa tcg aag acc ggt gga cct aat ggc tct atc agg aac gaa 363
 Asp Ala Gln Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu
 50 55 60
 gaa gag cac act cat ggt gcc aac agt ggt ttg aag atc gct ctc gat 411
 Glu Glu His Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp
 65 70 75
 ctc tgt ggtaggattt tgatttagtt tttgtagatt cactttctgg ataatttcat 467
 Leu Cys
 gcgatgtatc cgttttatgt tgtggtttta gaacactgtt caaaataatt acattatgct 527
 tttggaaatg gactttgtat cgcttaatta tgagatccta tctttgatgt ttca gag 584
 Glu
 80
 ggc gtg aaa gct aag cat ccc aaa atc aca tac gca gac ctg tat cag 632
 Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
 85 90 95
 gtgagttaag gctgtgagag aaatcttttt gatgtccttg ttgctttttc tgcacatttg 692
 tttttcaaag ttcgctggaa ctgtattcgg cttgtgtcat tacctcgtcc cagggttgag 752
 cttgttgttt aggagactta gttgatagtt gagcagctgt gtaaatatgg tttcagttgt 812
 aatttgtttc aggagatggt actgattgtg atttggttta caaaaatcat agattgacta 872
 tgttgttcaa ctagaacttt tatctcttgc agtaatagct aaattcaagt aaaatataca 932
 ctgaatgaat tcaaacgacc aagaaggaaa ctgtaatgta atgtcaatct gtttccatcc 992
 taagtcacat gtctgtcgtc tgtacctata acctgtctct acgactgttt gtattgccgt 1052
 ttctccattt tatatttggt ctacaagggt cgaggcttta tttatgaatt cccaatagaa 1112
 gtgtaccagt ttaatggcaa ttaagttttg ggtatgaatt atttactttt aagtgttttg 1172
 tttcag ctt gct ggt gtg gta gca gtt gag gtt act ggt gga cct gac 1220
 Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp
 100 105 110
 atc gtg ttc gtt ccc ggg aga aag g tatactttct catctcttga 1265

Ile Val Phe Val Pro Gly Arg Lys A
115

gacattataa cagcttatca gtttaacact aaagcaaaca taattactgt atgtttcttc 1325

ttgatagg at tca aat gtc tgc ccc aag gaa gga aga ctt cct gat gcc 1374
sp Ser Asn Val Cys Pro Lys Glu Gly Arg Leu Pro Asp Ala
120 125 130

aaa caa ggt acactaaatt cttgtatcaa ttataacaaa cttttcatgt 1423
Lys Gln Gly
135

tttctactga taatcttggt ttggaattgg aagatttttt ctatgaattc acattgttta 1483

tatctctgta ggt ttc caa cat ctc aga gat gtc ttc tac cgc atg gga 1532
Phe Gln His Leu Arg Asp Val Phe Tyr Arg Met Gly
140 145

cta tct gat aag gat att gtg gca ctc tca ggg ggt cat act ctg 1577
Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His Thr Leu
150 155 160

gtaaattcat tggtcactta cttaacttcc gttgtttttg aacaaatag cttgtgtgac 1637

ttatgaccac attgggtggt tag gga agg gct cac ccg gag agg tca ggc ttt 1690
Gly Arg Ala His Pro Glu Arg Ser Gly Phe
165 170

gat gga cca tgg acc caa gag ccg ctg aat ttt gac aac tcc tac ttc 1738
Asp Gly Pro Trp Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe
175 180 185

gt gtaattttca tttctttatc ctcagagatt ttctttgtgc atttttttaa 1790
Va

tctttctctgt ttgtgtctcc aagaaataaa agcagcaaac agatactttt ttacatgatc 1850

ggttatccat gattattttac tgttttggtta c c agg gaa ctg ctg aaa gga gaa 1903
1 Arg Glu Leu Leu Lys Gly Glu
190 195

tca gag ggc ttg ttg aaa ctt cca act gac aag acc tta ttg gaa gac 1951
Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr Leu Leu Glu Asp
200 205 210

ccg gag ttc cgt cgt ctt gtt gag ctt tat gca aaggtataat atactggaga 2004
Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala
215 220

tcttctctgc ctcttttgcca tttgtttctt gcgttgctat aataaccatt ggaacataac 2064

tcgatttcct ttattgggtt cacattttca ctgaatccac aagcacacac actgaatcac 2124

aaaccaaatt atctagggtt ttgttctaga gaacccacg gatccttatac gcctttatag 2184

ttgctgatgt tgcaaatga taaatgaac actcttacta ctatcagtga gaactgtaat 2244

attagctttt tgttagaacc gtaaacagaa attcctatgg ttctttatga tttccttgct 2304

taattaagtt tcaataagat aagaaagtgt tgttatgtgt tgacaagttc agtttgtggt 2364

ggcag gat gaa gat gca ttc ttc aga gac tac gcg gaa tcg cac aag aaa 2414
 Asp Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys
 225 230 235

ctc tct gag ctt ggt ttc aac cca aac tcc tca gca ggc aaa gca gtt 2462
 Leu Ser Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val
 240 245 250

gca gac agc acg att ctg gca cag agt gcg ttc ggg gtt gca gtt gct 2510
 Ala Asp Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala
 255 260 265 270

gct gcg gtt gtg gca ttt ggt tac ttt tac gag atc cgg aag agg atg 2558
 Ala Ala Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met
 275 280 285

aag taa acgaaatagg aagtaa 2580
 Lys

<210> 18

<211> 287

<212> PRT

<213> Arabidopsis thaliana

<400> 18

Met Ala Ala Pro Ile Val Asp Ala Glu Tyr Leu Lys Glu Ile Thr Lys
 1 5 10 15

Ala Arg Arg Glu Leu Arg Ser Leu Ile Ala Asn Lys Asn Cys Ala Pro
 20 25 30

Ile Met Leu Arg Leu Ala Trp His Asp Ala Gly Thr Tyr Asp Ala Gln
 35 40 45

Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu Glu Glu His
 50 55 60

Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp Leu Cys Glu
 65 70 75 80

Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
 85 90 95

Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp Ile Val
 100 105 110

Phe Val Pro Gly Arg Lys Asp Ser Asn Val Cys Pro Lys Glu Gly Arg
 115 120 125

Leu Pro Asp Ala Lys Gln Gly Phe Gln His Leu Arg Asp Val Phe Tyr
 130 135 140

Arg Met Gly Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His
 145 150 155 160
 Thr Leu Gly Arg Ala His Pro Glu Arg Ser Gly Phe Asp Gly Pro Trp
 165 170 175
 Thr Gln Glu Pro Leu Asn Phe Asp Asn Ser Tyr Phe Val Arg Glu Leu
 180 185 190
 Leu Lys Gly Glu Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr
 195 200 205
 Leu Leu Glu Asp Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala Asp
 210 215 220
 Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys Leu Ser
 225 230 235 240
 Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val Ala Asp
 245 250 255
 Ser Thr Ile Leu Ala Gln Ser Ala Phe Gly Val Ala Val Ala Ala Ala
 260 265 270
 Val Val Ala Phe Gly Tyr Phe Tyr Glu Ile Arg Lys Arg Met Lys
 275 280 285

<210> 19
 <211> 1861
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (26)..(284)

<220>
 <221> CDS
 <222> (541)..(917)

<220>
 <221> CDS
 <222> (1257)..(1493)

<220>
 <221> CDS
 <222> (1584)..(1853)

<400> 19
 atagaaaaac cctaagtagg ttgtg atg ttg cga gct tta gca cgg cct ctc 52
 Met Leu Arg Ala Leu Ala Arg Pro Leu
 1 5
 gaa cgg tgt ttg gga agc aga gct agt ggt gat ggt tta ctc tgg caa 100

Glu Arg Cys Leu Gly Ser Arg Ala Ser Gly Asp Gly Leu Leu Trp Gln
 10 15 20 25
 tcg gaa ttg aga cct cac gct ggc ggt gat tat tcg atc gcg gtg gtt 148
 Ser Glu Leu Arg Pro His Ala Gly Gly Asp Tyr Ser Ile Ala Val Val
 30 35 40
 caa gcc aat tcc agg ctt gaa gat cag agt cag gtt ttc aca tct tct 196
 Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser
 45 50 55
 tct gct act tac gtc ggt gta tac gat ggt cat ggt gga cct gaa gct 244
 Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Gly Pro Glu Ala
 60 65 70
 tct aga ttc gtt aac aga cat ctc ttt cct tat atg cac a gtaagttata 294
 Ser Arg Phe Val Asn Arg His Leu Phe Pro Tyr Met His L
 75 80 85
 atcccactct tccttccta aacttgtttt aggattcttt cttcttttga ctctttgact 354
 acgtttttga tggcctaaac ttatgagatc tctattaccc tgatcatttc aatattaaaa 414
 gattcgaaatt ttgctatgaa gttttggtct ttgtgaacat gttcagggttt gtaaattgcc 474
 tcttgaattg atttttagt catgttcttg ttagtgaaat ttacaggatt ggttttatga 534
 ttgcag aa ttt gca aga gaa cat ggg gga tta tct gta gat gtt atc aaa 584
 ys Phe Ala Arg Glu His Gly Gly Leu Ser Val Asp Val Ile Lys
 90 95 100
 aag gca ttc aaa gaa aca gaa gaa gag ttt tgt ggt atg gtt aaa cga 632
 Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys Gly Met Val Lys Arg
 105 110 115
 tcc ctt ccc atg aaa ccg caa atg gct act gta gga tct tgc tgt ctt 680
 Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly Ser Cys Cys Leu
 120 125 130
 gtt ggt gca atc tct aat gac aca ctg tat gtt gct aat ctt ggg gac 728
 Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala Asn Leu Gly Asp
 135 140 145
 tcg aga gcc gtt ctt gga agc gtt gtt tca ggg gtt gat agt aat aaa 776
 Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val Asp Ser Asn Lys
 150 155 160 165
 ggt gcc gta gct gaa cgg tta tct act gat cat aat gtt gct gtt gaa 824
 Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn Val Ala Val Glu
 170 175 180
 gaa gtg aga aag gag gtt aag gca ctt aac cct gat gac tca caa atc 872
 Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp Asp Ser Gln Ile
 185 190 195
 gtc tta tac aca cgt gga gtt tgg cgg att aaa ggc att att cag 917
 Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly Ile Ile Gln

200	205	210	
gtataactta gttttgcttg cctgcttggt aaattgcgtg tgattacata gcatctgtga			977
tgaagttata atatttaaaa ggtgtaatct gatgttggtt tttcttttct cttttcattt			1037
atataaatgg gggcttgcaa tgttccagga atccgtcaca cgggctcctg caacgtttct			1097
tccccagtggt attttgtgct tttctaagaa ttcccggtag tcagagctat acataataat			1157
gaagatacat gctttttagt tgcttgtgac ctttccgtga atgtttgagc tcgttgtata			1217
ttagtttagct aaatcgtttt catatacgct tctttatag gta tcg aga tca att			1271
		Val Ser Arg Ser Ile	215
ggg gat gta tac ttg aaa aaa ccg gag tat tac agg gac ccg att ttc			1319
Gly Asp Val Tyr Leu Lys Lys Pro Glu Tyr Tyr Arg Asp Pro Ile Phe			
220	225	230	
cag cga cat gga aat ccc att cct ttg agg aga ccc gcg atg aca gcc			1367
Gln Arg His Gly Asn Pro Ile Pro Leu Arg Arg Pro Ala Met Thr Ala			
235	240	245	
gaa ccc tcc att ata gta agg aag ctt aag cca cag gac ttg ttt ctg			1415
Glu Pro Ser Ile Ile Val Arg Lys Leu Lys Pro Gln Asp Leu Phe Leu			
250	255	260	265
ata ttt gca tca gat ggt ctc tgg gaa cat ctt agt gat gaa aca gcc			1463
Ile Phe Ala Ser Asp Gly Leu Trp Glu His Leu Ser Asp Glu Thr Ala			
270	275	280	
gta gaa atc gtc ctc aaa cac cca aga act gtaagttttc cctaaactca			1513
Val Glu Ile Val Leu Lys His Pro Arg Thr			
285	290		
agtttgcttt gtatcttcac atttatgtta gctacttagt ttattttattt attaactctg			1573
tgttctacag ggt att gcc cga aga ctt gta aga gct gct ctg gaa gaa			1622
Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu			
295	300		
gcg gca aag aag aga gaa atg aga tat gga gat ata aag aaa ata gcc			1670
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala			
305	310	315	320
aaa gga att cga cga cat ttc cat gac gac ata agc gtt att gta gtt			1718
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val			
325	330	335	
tat cta gat caa aac aaa acc agt tca tcg aat agt aaa ttg gtg aag			1766
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys			
340	345	350	
caa gga ggt atc acc gct cca ccg gat atc tac tca tta cac tct gat			1814
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp			
355	360	365	

gaa gca gag caa cga cgg tta ctc aat gtg tta tac tga ctgtttga 1861
 Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
 370 375 380

<210> 20

<211> 380

<212> PRT

<213> Arabidopsis thaliana

<400> 20

Met Leu Arg Ala Leu Ala Arg Pro Leu Glu Arg Cys Leu Gly Ser Arg
 1 5 10 15

Ala Ser Gly Asp Gly Leu Leu Trp Gln Ser Glu Leu Arg Pro His Ala
 20 25 30

Gly Gly Asp Tyr Ser Ile Ala Val Val Gln Ala Asn Ser Arg Leu Glu
 35 40 45

Asp Gln Ser Gln Val Phe Thr Ser Ser Ser Ala Thr Tyr Val Gly Val
 50 55 60

Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
 65 70 75 80

Leu Phe Pro Tyr Met His Lys Phe Ala Arg Glu His Gly Gly Leu Ser
 85 90 95

Val Asp Val Ile Lys Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys
 100 105 110

Gly Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val
 115 120 125

Gly Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val
 130 135 140

Ala Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly
 145 150 155 160

Val Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His
 165 170 175

Asn Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro
 180 185 190

Asp Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys
 195 200 205

Gly Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys
 210 215 220

Pro Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile
 225 230 235 240

Pro Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg
 245 250 255
 Lys Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu
 260 265 270
 Trp Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His
 275 280 285
 Pro Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
 290 295 300
 Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
 305 310 315 320
 Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
 325 330 335
 Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
 340 345 350
 Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
 355 360 365
 Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
 370 375 380

<210> 21
 <211> 3633
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (41)..(356)

<220>
 <221> CDS
 <222> (811)..(956)

<220>
 <221> CDS
 <222> (1076)..(1389)

<220>
 <221> CDS
 <222> (1544)..(1592)

<220>
 <221> CDS
 <222> (1925)..(2010)

<220>
 <221> CDS
 <222> (2037)..(2120)

gag gag aag cag c gtagagtttt agaaggctcg aaaatgggttc gcattctgat 396
Glu Glu Lys Gln A
105

tcaattgcat gcttagttcg ttgattttc ttagatatgt tactgtttta gggtggggtt 456
 ttcaagttta tgctaaagtt tggctttttt tgagtacatt tatgtgtatc ttactaggtc 516
 ttacctcata gtccaagcta gattcgagct catttatgtg tatgatctat agtcacagaa 576
 catctatgtg ttcgagctca tttatgtgtt tgaatatgaa tatgatgcta caaaagactt 636
 ttttggcagg aggtggacag aagttctaag gtcgtgtctt cgactagctc aggtattctt 696
 gggtggataat gttaaagtgt ttgctttcta acatagtggg tcatttttct gtatgggttt 756
 tcgatttatc ttccattttt tggacttaag ttgatgagc catgtttcat gtag gt 812
 rg
 tca gat gtt tta ccg caa gga aat gca gtt tca aaa gat acc tct aga 860
 Ser Asp Val Leu Pro Gln Gly Asn Ala Val Ser Lys Asp Thr Ser Arg
 110 115 120
 ggg aat gca gac tca aaa gac acc tct aga caa ggg aat gca gat tca 908
 Gly Asn Ala Asp Ser Lys Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser
 125 130 135
 aaa gaa gtc tca cgg tca aca ttt tct gcg gtt ttc agt aaa cca aaa 956
 Lys Glu Val Ser Arg Ser Thr Phe Ser Ala Val Phe Ser Lys Pro Lys
 140 145 150
 gtatggagca tcgttttttt tttttgttc aacgtatgga gcctctatat ttgcaattt 1016
 taaaactggt ttggatgggt acttcttcat gatacgattt tgtaatctgt gttcaacag 1075
 acg gat tct cag tca aag aaa gcc ttt ggt aaa gaa cta gaa gat ctg 1123
 Thr Asp Ser Gln Ser Lys Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu
 155 160 165 170
 gga tgt gaa agg agg aaa cac aag gct ggt aga aag cct gta aca agg 1171
 Gly Cys Glu Arg Arg Lys His Lys Ala Gly Arg Lys Pro Val Thr Arg
 175 180 185
 ctg agc aac ggg tgg cgg ttg ttg cca gat gta ggg aaa gct gag cac 1219
 Leu Ser Asn Gly Trp Arg Leu Leu Pro Asp Val Gly Lys Ala Glu His
 190 195 200
 agt gca aag cag ttt gat tct gga ctt aaa gaa tca aaa ggg aat aag 1267
 Ser Ala Lys Gln Phe Asp Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys
 205 210 215
 aaa tcc aag gaa cct tat gga aag aaa agg ccc atg gaa tct tcg act 1315
 Lys Ser Lys Glu Pro Tyr Gly Lys Lys Arg Pro Met Glu Ser Ser Thr
 220 225 230
 tat tct ctg att gat gat gat gat gat gat gat gat gat gac aac 1363
 Tyr Ser Leu Ile Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn
 235 240 245 250
 gac acc agt ggc cat gaa act cct ag gtctgtttcc aactgtttct 1409

Asp Thr Ser Gly His Glu Thr Pro Ar
255

gctactagtt tgttggtttc tctaagggtt ctcaagttta ccaactgctgg ttactgcaat 1469

tttggttgga catgacaatc tggtagataa tagaatgaga tgtattgtaa ttgctcaact 1529

tctttctctc atag g gag tgg tct tgg gaa aaa tct cca tca caa agt tca 1580
g Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser
260 265 270

agg cgc cgt aag gtattcttgc ttactccgc tactgtatat cttgcaattg 1632
Arg Arg Arg Lys
275

cagtttttac gtagtcatta tagtccttaa gaaattttaca ccagcagaag catgactcat 1692

tttctaaacc ttcttggtat ctcccaacag aaaattttat gaattcctta aaaagacttc 1752

agttttcgaa cgttgattc ctctctagat gaactgcagg atttatactt gccaggaaaa 1812

cttctactt gactatatca tttatttggc ttctttaata ttgtctttac tccaactcat 1872

ttgttatggt gtttttctta cttattgatg atattcccta aaaaaactat ag aaa tca 1930
Lys Ser

gag gac aca gtg ata aat gtg gat gaa gaa gaa gct cag cct tca aca 1978
Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu Ala Gln Pro Ser Thr
280 285 290

gtg gcg gag caa gcg gct gaa ctg cct gaa gg gtaaagtga cctattttct 2030
Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gl
295 300

ctttag c ctc att aag tta caa ctg gct ata tat aaa cta ata gtt gat 2079
y Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp
305 310 315

aaa aca tgc agc tta cag gaa gat ata tgc tac cca aca ag gtaaacttat 2130
Lys Thr Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSe
320 325 330 e

ctcaagactg atctaggcta acttcctgta aatttgtaac cctcaaaaga tttaatgctt 2190

ggtgattcag ggatgatcct cactttgttc aagtttgtct taaagatctt gaatgccttg 2250

cacctcgaga atatctgaca tcgccggtta tgaatttcta catgaggtat tttttggagt 2310

gatagacttg ccatatatgt catcttatat tatgctagcg ctatttgcat gttatttata 2370

taactattgt cctgttttct tttggtag g ttc ttg cag cag cag ata tca tca 2423
g Phe Leu Gln Gln Gln Ile Ser S
h 335 340

tcg aat caa atc tct gct gat tgt cac ttc ttt aat acc tat ttc tac 2471
r Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe Asn Thr Tyr Phe T
345 350 355

aag aag ctc agt gac gct gtt acg tac aag gtgattagaa aaatgtgatc 2521
r Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys
360 365

ctttaaaaat aattatctgt tggcattctt gcgattcaaa tttttatcat tggtatttat 2581

gttaactgggt ctatttatct tgcctttca atgaaatag ggg aat gac aag gat 2635
Gly Asn Asp Lys A
370

gcc ttc ttt gtg agg ttc agg cgg tgg tgg aag ggt att gat cta ttt 2683
p Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly Ile Asp Leu P
375 380 385

cgt aag gct tat att ttc ata cca ata cat gaa ga gtaagtatct 2728
e Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu
390 395

ttccttttag cactctactt tcgatttttt cgcaagagtt ctcaagaatt cagattcttg 2788

taccatgttt cag t ctc cac tgg agc ctt gtg ata gtt tgc atc cct gat 2838
r Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp
e 400s 405 410

aag aaa gat gaa tcg ggg ttg act ata ctt cac ctt gat tct cta gga 2886
Lys Lys Asp Glu Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly
415 420 425

ctt cac tcg aga aaa tca att gtt gaa aat gta aaa ag gtgagatgct 2934
Leu His Ser Arg Lys Ser Ile Val Glu Asn Val Lys Ar
430 435

aggggcttta cccgtgactt tatgttttca catgcttgac gttgtatgca tatggtttca 2994

gttcataaaaa ggaaaaatta ttacactggc ttgaaaatgt acgacattta ctagttttcta 3054

tgtcaatttg ttgtag g ttt cta aaa gac gaa tgg aat tat ttg aat caa 3104
g Phe Leu Lys Asp Glu Trp Asn Tyr Leu Asn Gln
440 445 450

gat gac tat tcc ttg gat ctg cct atc tca gaa aaa gta tgg aaa aac 3152
Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys Val Trp Lys Asn
455 460 465

ctc cct cgt agg atc agc gaa gct gtt gtt cag gtcagtcttt taccttctta 3205
Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln
470 475

atcccatgat tcaaggaact ttgtttatcac gggtttcttcg gaaatatgat tatattcaga 3265

cactagaacc acaggaagtt caattcgtct tatgatatta ttctctttgt gcaaccag 3323

gtt ccg cag cag aaa aac gat ttt gat tgt ggt ccg ttt gtg ctc ttc 3371
Val Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe
480 485 490

ttc att aaa cgg ttc att gaa gag gcg cct caa agg ctg aaa agg aaa 3419
 Phe Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys
 495 500 505

gac ctg gga atg gtgagtaatc tcaaactctt ttcctgatac cgaatcacat 3471
 Asp Leu Gly Met
 510

atcttcttctt tactcttgtc taaacttggt tctcaatgt atccag ttc gac aag 3526
 Phe Asp Lys
 515

aag tgg ttt aga ccc gat gaa gcc tct gct ctg aga atc aaa atc cga 3574
 Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala Leu Arg Ile Lys Ile Arg
 520 525 530

aac acg ctg atc gag cta ttc cgt gtc agt gac cag aca gag taa 3619
 Asn Thr Leu Ile Glu Leu Phe Arg Val Ser Asp Gln Thr Glu
 535 540 545

accagtacag atta 3633

<210> 22
 <211> 546
 <212> PRT
 <213> Arabidopsis thaliana

<400> 22
 Met Thr Lys Arg Lys Lys Glu Val Ile Asp Val Asp Cys Ser Glu Lys
 1 5 10 15

Lys Asp Phe Val Ile Asp Trp Ser Ser Ala Met Asp Lys Glu Asp Glu
 20 25 30

Val Pro Glu Leu Glu Ile Val Asn Thr Thr Lys Pro Thr Pro Pro
 35 40 45

Pro Pro Thr Phe Phe Ser Asp Asp Gln Thr Asp Ser Pro Lys Leu Leu
 50 55 60

Thr Asp Arg Asp Leu Asp Glu Gln Leu Glu Arg Lys Lys Ala Ile Leu
 65 70 75 80

Thr Leu Gly Pro Gly Leu Pro Asp Lys Gly Glu Lys Ile Arg Leu Lys
 85 90 95

Ile Ala Asp Leu Glu Glu Glu Lys Gln Arg Ser Asp Val Leu Pro Gln
 100 105 110

Gly Asn Ala Val Ser Lys Asp Thr Ser Arg Gly Asn Ala Asp Ser Lys
 115 120 125

Asp Thr Ser Arg Gln Gly Asn Ala Asp Ser Lys Glu Val Ser Arg Ser
 130 135 140

Thr Phe Ser Ala Val Phe Ser Lys Pro Lys Thr Asp Ser Gln Ser Lys

145 150 155 160
 Lys Ala Phe Gly Lys Glu Leu Glu Asp Leu Gly Cys Glu Arg Arg Lys
 165 170 175
 His Lys Ala Gly Arg Lys Pro Val Thr Arg Leu Ser Asn Gly Trp Arg
 180 185 190
 Leu Leu Pro Asp Val Gly Lys Ala Glu His Ser Ala Lys Gln Phe Asp
 195 200 205
 Ser Gly Leu Lys Glu Ser Lys Gly Asn Lys Lys Ser Lys Glu Pro Tyr
 210 215 220
 Gly Lys Lys Arg Pro Met Glu Ser Ser Thr Tyr Ser Leu Ile Asp Asp
 225 230 235 240
 Asp Asp Asp Asp Asp Asp Asp Asp Asp Asn Asp Thr Ser Gly His Glu
 245 250 255
 Thr Pro Arg Glu Trp Ser Trp Glu Lys Ser Pro Ser Gln Ser Ser Arg
 260 265 270
 Arg Arg Lys Lys Ser Glu Asp Thr Val Ile Asn Val Asp Glu Glu Glu
 275 280 285
 Ala Gln Pro Ser Thr Val Ala Glu Gln Ala Ala Glu Leu Pro Glu Gly
 290 295 300
 Leu Ile Lys Leu Gln Leu Ala Ile Tyr Lys Leu Ile Val Asp Lys Thr
 305 310 315 320
 Cys Ser Leu Gln Glu Asp Ile Cys Tyr Pro Thr ArSeg Phe Leu Gln
 325 330 e 335
 Gln Gln Ile Ser Sr Ser Asn Gln Ile Ser Ala Asp Cys His Phe Phe
 340e 345 350
 Asn Thr Tyr Phe Tr Lys Lys Leu Ser Asp Ala Val Thr Tyr Lys Gly
 355y 360 365
 Asn Asp Lys Ap Ala Phe Phe Val Arg Phe Arg Arg Trp Trp Lys Gly
 370 375 380
 Ile Asp Leu Pe Arg Lys Ala Tyr Ile Phe Ile Pro Ile His Glu r
 385 390 395u
 Leu His Trp Ser Leu Val Ile Val Cys Ile Pro Asp Lys Lys Asp Glu
 400 405 410
 Ser Gly Leu Thr Ile Leu His Leu Asp Ser Leu Gly Leu His Ser Arg
 415 420 425
 Lys Ser Ile Val Glu Asn Val Lys Arg Phe Leu Lys Asp Glu Trp Asn
 430 435 440
 Tyr Leu Asn Gln Asp Asp Tyr Ser Leu Asp Leu Pro Ile Ser Glu Lys

445 450 455 460
 Val Trp Lys Asn Leu Pro Arg Arg Ile Ser Glu Ala Val Val Gln Val
 465 470 475
 Pro Gln Gln Lys Asn Asp Phe Asp Cys Gly Pro Phe Val Leu Phe Phe
 480 485 490
 Ile Lys Arg Phe Ile Glu Glu Ala Pro Gln Arg Leu Lys Arg Lys Asp
 495 500 505
 Leu Gly Met Phe Asp Lys Lys Trp Phe Arg Pro Asp Glu Ala Ser Ala
 510 515 520
 Leu Arg Ile Lys Ile Arg Asn Thr Leu Ile Glu Leu Phe Arg Val Ser
 525 530 535 540
 Asp Gln Thr Glu

<210> 23
 <211> 1108
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (22)..(1107)

<400> 23
 aggagttaga gcatcatcaa g atg aag gca ctc att ctt gtt gga ggc ttc 51
 Met Lys Ala Leu Ile Leu Val Gly Gly Phe
 1 5 10
 ggc act cgc ttg aga cca ttg act ctc agt ttc cca aag ccc ctt gtt 99
 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val
 15 20 25
 gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag 147
 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys
 30 35 40
 gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu
 45 50 55
 gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys
 60 65 70
 atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu
 75 80 85 90
 gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe

95	100	105	
gtt ctt aac agt gat gtg att agt gag tac cct ctt aaa gaa atg ctt Val Leu Asn Ser Asp Val Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu 110 115 120			387
gag ttt cac aaa tct cac ggt ggg gaa gcc tcc ata atg gta aca aag Glu Phe His Lys Ser His Gly Gly Glu Ala Ser Ile Met Val Thr Lys 125 130 135			435
gtg gat gaa ccg tcg aaa tat gga gtg gtt gtt atg gaa gaa agc act Val Asp Glu Pro Ser Lys Tyr Gly Val Val Val Met Glu Glu Ser Thr 140 145 150			483
gga aga gtg gag aag ttt gtg gaa aag cca aaa ctg tat gta ggt aac Gly Arg Val Glu Lys Phe Val Glu Lys Pro Lys Leu Tyr Val Gly Asn 155 160 165 170			531
aag atc aac gct ggg att tat ctt ctg aac cca tct gtt ctt gat aag Lys Ile Asn Ala Gly Ile Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys 175 180 185			579
att gag cta aga ccg act tca atc gaa aaa gag act ttc cct aag att Ile Glu Leu Arg Pro Thr Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile 190 195 200			627
gca gca gcg caa ggg ctc tat gct atg gtg cta cca ggg ttt tgg atg Ala Ala Ala Gln Gly Leu Tyr Ala Met Val Leu Pro Gly Phe Trp Met 205 210 215			675
gac att ggg caa ccc cgt gac tac ata acg ggt ttg aga ctc tac tta Asp Ile Gly Gln Pro Arg Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu 220 225 230			723
gac tcc ctt agg aag aaa tct cct gcc aaa tta acc agt ggg cca cac Asp Ser Leu Arg Lys Lys Ser Pro Ala Lys Leu Thr Ser Gly Pro His 235 240 245 250			771
ata gtt ggg aat gtt ctt gtt gac gaa acc gct aca att ggg gaa gga Ile Val Gly Asn Val Leu Val Asp Glu Thr Ala Thr Ile Gly Glu Gly 255 260 265			819
tgt ttg att gga cca gac gtt gcc att ggt cca ggc tgc att gtt gag Cys Leu Ile Gly Pro Asp Val Ala Ile Gly Pro Gly Cys Ile Val Glu 270 275 280			867
tca gga gtc aga ctc tcc cga tgc acg gtc atg cgt gga gtc cgc atc Ser Gly Val Arg Leu Ser Arg Cys Thr Val Met Arg Gly Val Arg Ile 285 290 295			915
aag aag cat gcg tgt atc tcg agc agt atc atc ggg tgg cac tca acg Lys Lys His Ala Cys Ile Ser Ser Ser Ile Ile Gly Trp His Ser Thr 300 305 310			963
gtt ggt caa tgg gcc agg atc gag aac atg acg atc ctc ggt gag gat Val Gly Gln Trp Ala Arg Ile Glu Asn Met Thr Ile Leu Gly Glu Asp 315 320 325 330			1011

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107
 His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met
 350 355 360

aa 1109

<210> 24

<211> 361

<212> PRT

<213> Arabidopsis thaliana

<400> 24

Met Lys Ala Leu Ile Leu Val Gly Gly Phe Gly Thr Arg Leu Arg Pro
 1 5 10 15

Leu Thr Leu Ser Phe Pro Lys Pro Leu Val Asp Phe Ala Asn Lys Pro
 20 25 30

Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu
 35 40 45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu
 50 55 60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu
 65 70 75 80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys
 85 90 95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val
 100 105 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His
 115 120 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys
 130 135 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe
 145 150 155 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile
 165 170 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr
 180 185 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu
 195 200 205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
 210 215 220
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
 225 230 235 240
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
 245 250 255
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
 260 265 270
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
 275 280 285
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
 290 295 300
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
 305 310 315 320
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
 325 330 335
 Ile Tyr Ser Asn Gly Gly Val Val Leu Pro His Lys Glu Ile Lys Ser
 340 345 350
 Asn Ile Leu Lys Pro Glu Ile Val Met
 355 360

<210> 25
 <211> 1071
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (9)..(1055)

<400> 25
 tccaataa atg aaa gca act cta gca gca ccc tct tct ctc aca agc ctc 50
 Met Lys Ala Thr Leu Ala Ala Pro Ser Ser Leu Thr Ser Leu
 1 5 10
 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15 20 25 30
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146
 Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
 35 40 45
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat gcc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser ggt His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att gcc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
 290 295 300
 tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
 305 310 315
 att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
 320 325 330
 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055
 Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 335 340 345
 gtctaaagct atacta 1071

<210> 26
 <211> 348
 <212> PRT
 <213> Arabidopsis thaliana

<400> 26
 Met Lys Ala Thr Leu Ala Ala Pro Ser Ser Leu Thr Ser Leu Pro Tyr
 1 5 10 15
 Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe Arg Ser
 20 25 30
 Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val
 35 40 45
 Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
 50 55 60
 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
 65 70 75 80
 Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
 85 90 95
 Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
 100 105 110
 Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
 115 120 125
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
 130 135 140
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
 145 150 155 160
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
 180 185 190
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
 195 200 205
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
 210 215 220
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
 225 230 235 240
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
 245 250 255
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
 260 265 270
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
 275 280 285
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
 290 295 300
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
 305 310 315 320
 Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
 325 330 335
 Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 340 345

<210> 27
 <211> 768
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (3)..(752)

<400> 27
 ag atg aag ttc aac gtt gcg aat cca act act gga tgc cag aag aag 47
 Met Lys Phe Asn Val Ala Asn Pro Thr Thr Gly Cys Gln Lys Lys
 1 5 10 15
 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95
 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
 20 25 30
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg	191
Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met	
50 55 60	
aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga	239
Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg	
65 70 75	
gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga	287
Gly Thr Pro Cys Phe Arg Gly His Gly Arg Thr Gly Glu Arg Arg	
80 85 90 95	
aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg	335
Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu	
100 105 110	
aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc	383
Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr	
115 120 125	
gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt	431
Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg	
130 135 140	
aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac	479
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn	
145 150 155	
act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa	527
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys	
160 165 170 175	
gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag	575
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys	
180 185 190	
aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct	623
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser	
195 200 205	
gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag	671
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln	
210 215 220	
cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct	719
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser	
225 230 235	
tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca	768
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala	
240 245 250	

<210> 28

<211> 249

<212> PRT

<213> Arabidopsis thaliana

<400> 28

```

Met Lys Phe Asn Val Ala Asn Pro Thr Thr Gly Cys Gln Lys Lys Leu
  1           5           10           15
Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg Ile
          20           25           30
Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
      35           40           45
Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
      50           55           60
Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
      65           70           75           80
Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
          85           90           95
Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
          100          105          110
Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
          115          120          125
His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
          130          135          140
Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
          145          150          155          160
Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
          165          170          175
Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
          180          185          190
Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
          195          200          205
Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
          210          215          220
Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser
          225          230          235          240
Ala Ala Ala Lys Pro Ser Val Thr Ala
          245

```

<210> 29

<211> 1201

<212> DNA

<213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (24) .. (35)

<220>
 <221> CDS
 <222> (147) .. (187)

<220>
 <221> CDS
 <222> (283) .. (383)

<220>
 <221> CDS
 <222> (689) .. (833)

<220>
 <221> CDS
 <222> (916) .. (1005)

<220>
 <221> CDS
 <222> (1103) .. (1196)

<400> 29
 cacgcgggag ctcaacatca gcc atg gcg gaa cag gttactcgat ctgttctctc 55
 Met Ala Glu Gln
 1

ctctaagctt atcctcgttt tatgatctat tgatccttat tcaactcaaat gattctaata 115

ctcttctctt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
 Thr Glu Lys Ala Phe Leu Lys
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217
 Gln Pro Lys Val Phe Leu Se
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
 35 40 45

gcc att gat g gtatgtttta gcttttaact cggtataata gataaggaac 423
 Ala Ile Asp G
 50

tcttggattg tgttgttcat atagtcgata gatttcaaat gctattttgt cttgtagaat 483

cttaagcttt ggtttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

```
<210> 30
<211> 160
<212> PRT
<213> Arabidopsis thaliana
```

<400> 30
Met Ala Glu Gln Thr Glu Lys Ala Phe Leu Lys Gln Pro Lys Val
1 5 10 15

Phe Leu Ser Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly
 20 25 30
 Gly Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg
 35 40 45
 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
 50 55 60
 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
 65 70 75 8
 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val
 85 90 95
 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His
 100 105 110
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
 115 120 125
 Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val
 130 135 140
 Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly
 145 150 155 16
 Met

<210> 31
 <211> 1790
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (23)..(1780)

<400> 31
 tgtgagtaat ttagcgaaaa cg atg ggt tcc atc gaa gaa gaa gca aga cct 52
 Met Gly Ser Ile Glu Glu Glu Ala Arg Pro
 1 5 10
 ctc atc gaa gaa ggt tta att tta cag gaa gtg aaa ttg tat gct gaa 100
 Leu Ile Glu Glu Gly Leu Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu
 15 20 25
 gat ggt tca gtg gac ttt aat gga aac cca cca ttg aag gag aaa aca 148
 Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr
 30 35 40
 gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196
 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
 45 50 55

agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc	244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr	
60 65 70	
act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca	292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr	
75 80 85 90	
tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct	340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala	
95 100 105	
gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att	388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile	
110 115 120	
tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca	436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala	
125 130 135	
ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca	484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro	
140 145 150	
gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga	532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly	
155 160 165 170	
act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt	580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe	
175 180 185	
gat gac acg gac tct ccg gaa cga gtt aga aaa gct tcg ttc ttt aac	628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn	
190 195 200	
tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt	676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu	
205 210 215	
cta gtt tgg att caa gag aat ccg ggg tgg ggt tta ggg ttt ggg ata	724
Leu Val Trp Ile Gln Glu Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile	
220 225 230	
cca aca gtg ttc atg gga cta gcc att gca agt ttc ttc ttt ggc aca	772
Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr	
235 240 245 250	
cct ctt tat agg ttt cag aaa cct gga gga agc cct ata act cgg att	820
Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile	
255 260 265	
tcc caa gtc gtg gtt gct tcg ttc ccg aaa tcg tct gtc aaa gtc cct	868
Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro	
270 275 280	
gaa gac gcc aca ctt ctg tat gaa act caa gac aag aac tct gct att	916

Glu Asp Ala Thr Leu Leu Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile	
285 290 295	
gct gga agt aga aaa atc gag cat acc gat gat tgc cag tat ctt gac	964
Ala Gly Ser Arg Lys Ile Glu His Thr Asp Asp Cys Gln Tyr Leu Asp	
300 305 310	
aaa gcc gct gtt atc tca gaa gaa gaa tcg aaa tcc gga gat tat tcc	1012
Lys Ala Ala Val Ile Ser Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser	
315 320 325 330	
aac tcg tgg aga cta tgc acg gtt acg caa gtc gaa gaa ctc aag att	1060
Asn Ser Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile	
335 340 345	
ctg atc cga atg ttc cca atc tgg gct tct ggt atc att ttc tca gct	1108
Leu Ile Arg Met Phe Pro Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala	
350 355 360	
gta tac gca caa atg tcc aca atg ttt gtt caa caa ggc cga gcc atg	1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met	
365 370 375	
aac tgc aaa att gga tca ttc cag ctt cct cct gca gca ctc ggg aca	1204
Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr	
380 385 390	
ttc gac aca gca agc gtc atc atc tgg gtg ccg ctc tac gac cgg ttc	1252
Phe Asp Thr Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe	
395 400 405 410	
atc gtt ccc tta gca aga aag ttc aca gga gta gac aaa gga ttc act	1300
Ile Val Pro Leu Ala Arg Lys Phe Thr Gly Val Asp Lys Gly Phe Thr	
415 420 425	
gag ata caa aga atg gga att ggt ctg ttt gtc tct gtt ctc tgt atg	1348
Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met	
430 435 440	
gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat	1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp	
445 450 455	
ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg	1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp	
460 465 470	
cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc	1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe	
475 480 485 490	
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga	1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg	
495 500 505	
agc ttg tgc agt gcc tta gct ctt ttg acc aat gca ctt ggt aac tac	1588
Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr	

510 515 520
 ttg agc tcg ttg atc ctc acg ctc gtg act tat ttt aca aca aga aat 1636
 Leu Ser Ser Leu Ile Leu Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn
 525 530 535
 ggg caa gaa ggt tgg att tcg gat aat ctc aat tca ggt cat ctc gat 1684
 Gly Gln Glu Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp
 540 545 550
 tac ttc ttc tgg ctc ttg gct ggt ctt agc ctt gtg aac atg gcg gtt 1732
 Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val
 555 560 565 570
 tac ttc ttc tct gct gct agg tat aag caa aag aaa gct tcg tcg tag 1780
 Tyr Phe Phe Ser Ala Ala Arg Tyr Lys Gln Lys Lys Ala Ser Ser
 575 580 585
 taatgctggt a 1791

<210> 32
 <211> 585
 <212> PRT
 <213> Arabidopsis thaliana

<400> 32
 Met Gly Ser Ile Glu Glu Ala Arg Pro Leu Ile Glu Glu Gly Leu
 1 5 10 15
 Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu Asp Gly Ser Val Asp Phe
 20 25 30
 Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr Gly Asn Trp Lys Ala Cys
 35 40 45
 Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly
 50 55 60
 Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly
 65 70 75 80
 Asn Val Ser Ala Ala Thr Asn Val Thr Thr Trp Gln Gly Thr Cys Tyr
 85 90 95
 Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg
 100 105 110
 Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser
 115 120 125
 Ala Leu Thr Leu Ser Ala Ser Val Pro Ala Leu Lys Pro Ala Glu Cys
 130 135 140
 Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr Ala Met Phe
 145 150 155 160

Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
 165 170 175
 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
 180 185 190
 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
 195 200 205
 Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu
 210 215 220
 Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
 225 230 235 240
 Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln
 245 250 255
 Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala
 260 265 270
 Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu
 275 280 285
 Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile
 290 295 300
 Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser
 305 310 315 320
 Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser Asn Ser Trp Arg Leu Cys
 325 330 335
 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
 340 345 350
 Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
 355 360 365
 Thr Met Phe Val Gln Gln Gly Arg Ala Met Asn Cys Lys Ile Gly Ser
 370 375 380
 Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
 385 390 395 400
 Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro Leu Ala Arg
 405 410 415
 Lys Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln Arg Met Gly
 420 425 430
 Ile Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala Ala Ile Val
 435 440 445
 Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser
 450 455 460

Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe
 465 470 475 480
 Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe
 485 490 495
 Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
 500 505 510
 Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu
 515 520 525
 Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gln Glu Gly Trp Ile
 530 535 540
 Ser Asp Asn Leu Asn Ser Gly His Leu Asp Tyr Phe Phe Trp Leu Leu
 545 550 555 560
 Ala Gly Leu Ser Leu Val Asn Met Ala Val Tyr Phe Phe Ser Ala Ala
 565 570 575
 Arg Tyr Lys Gln Lys Lys Ala Ser Ser
 580 585

<210> 33
 <211> 1984
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(1975)

<400> 33
 ttcaccggtcg gcttctcaa atg cag gat att ctc gga tcg gtt cgc cga tcc 52
 Met Gln Asp Ile Leu Gly Ser Val Arg Arg Ser
 1 5 10
 ttg gtt ttc cgg tcg tct ttg gcc gga gac gat ggt act agc ggc gga 100
 Leu Val Phe Arg Ser Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly
 15 20 25
 ggt ctt agc gga ttc gtc ggg aag att aac tct agt atc cgt agc tct 148
 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
 30 35 40
 cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga 196
 Arg Ile Gly Leu Phe Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg
 45 50 55
 aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt 244
 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
 60 65 70 75
 tgc ggt gct ttt gga aga gtt tac atg gga atg aac ctc gat tcc ggc 292

Cys Gly Ala Phe Gly Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly	
80 85 90	
gag ctt ctt gca att aaa cag gtt tta atc gct cca agc agt gct tca	340
Glu Leu Leu Ala Ile Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser	
95 100 105	
aag gag aag act cag ggt cac atc cga gag ctt gag gaa gaa gta caa	388
Lys Glu Lys Thr Gln Gly His Ile Arg Glu Leu Glu Glu Glu Val Gln	
110 115 120	
ctt ctt aag aat ctt tca cat ccg aac atc gtt aga tac ttg ggt act	436
Leu Leu Lys Asn Leu Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr	
125 130 135	
gta aga gag agt gat tcg ttg aat att ttg atg gag ttt gtt cct ggt	484
Val Arg Glu Ser Asp Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly	
140 145 150 155	
gga tca ata tca tct ttg ttg gag aag ttt gga tct ttt cct gag cct	532
Gly Ser Ile Ser Ser Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro	
160 165 170	
gtg att att atg tac aca aag caa ctt ctg ctt ggg ctg gaa tat ctt	580
Val Ile Ile Met Tyr Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu	
175 180 185	
cac aac aat ggg atc atg cat cga gat att aag ggg gca aat att ttg	628
His Asn Asn Gly Ile Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu	
190 195 200	
gtc gat aac aaa ggt tgc atc aga ctc gca gat ttt ggt gct tcc aag	676
Val Asp Asn Lys Gly Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys	
205 210 215	
aaa gtt gta gag cta gct act gta aat ggt gcc aaa tct atg aag ggg	724
Lys Val Val Glu Leu Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly	
220 225 230 235	
acg cct tat tgg atg gct cct gaa gtc att ctc cag act ggt cat agc	772
Thr Pro Tyr Trp Met Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser	
240 245 250	
ttc tct gct gat ata tgg agt gtt ggg tgc act gtg att gag atg gct	820
Phe Ser Ala Asp Ile Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala	
255 260 265	
acg ggg aag cct ccc tgg agc gag cag tat cag cag ttt gct gct gtc	868
Thr Gly Lys Pro Pro Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val	
270 275 280	
ctt cat att ggt aga aca aaa gct cat cct cca att cca gaa gac ctc	916
Leu His Ile Gly Arg Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu	
285 290 295	
tca cca gag gct aaa gac ttt cta atg aaa tgc tta cac aaa gaa cca	964
Ser Pro Glu Ala Lys Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro	

300	305	310	315	
agc ttg aga ctc tct gca acc gaa ttg ctt cag cac ccg ttt gtc act				1012
Ser Leu Arg Leu	Ser Ala Thr Glu Leu	Leu Gln His Pro Phe	Val Thr	
	320	325	330	
gga aag cgc cag gaa cct tat cca gct tac cgt aat tct ctt acg gaa				1060
Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu				
	335	340	345	
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata				1108
Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile				
	350	355	360	
aat tcg ttg atc agg agg tcg aca tgt tca ggc ttg aag gat gtc tgt				1156
Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys				
	365	370	375	
gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat				1204
Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn				
	380	385	390	395
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln				
	400	405	410	
acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt				1300
Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val				
	415	420	425	
ttg tca cag tcc acc gat tta aac aag agt ttt aat ccc atg tgt gat				1348
Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp				
	430	435	440	
tcc acg gat aac tgg tct tgc aag ttt gat gaa agc cca aaa gtg atg				1396
Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met				
	445	450	455	
aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act				1444
Lys Ser Lys Ser Asn Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr				
	460	465	470	475
gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct				1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser				
	480	485	490	
tcc gtt gca gag gat gat tat aaa ggc aca gag ttg aaa ata aaa tca				1540
Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser				
	495	500	505	
ttt ttg gat gag aag gct cag gat ttg aaa agg ttg cag acc cct ctg				1588
Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu				
	510	515	520	
ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca				1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala				
	525	530	535	

ctt gga gac acc aat atc tac aat tta cca aac tta cca agt ata agc 1684
 Leu Gly Asp Thr Asn Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser
 540 545 550 555

aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
 Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
 560 565 570

gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
 Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
 575 580 585

aga gtg atg cag tca gga act gaa cca act caa gtc aac gag tcg acc 1828
 Arg Val Met Gln Ser Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr
 590 595 600

aag aag gga gta aat aat agc cgt tgt ttc tca gag ata cgt cgg aag 1876
 Lys Lys Gly Val Asn Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys
 605 610 615

tgg gaa gaa gaa ctc tat gaa gag ctt gag agg cat cga gag aat ctg 1924
 Trp Glu Glu Glu Leu Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu
 620 625 630 635

cga cac gct ggt gca gga ggg aag act cca tta tca ggc cac aaa gga 1972
 Arg His Ala Gly Ala Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
 640 645 650

tag tgaacggct 1984

<210> 34
 <211> 651
 <212> PRT
 <213> Arabidopsis thaliana

<400> 34
 Met Gln Asp Ile Leu Gly Ser Val Arg Arg Ser Leu Val Phe Arg Ser
 1 5 10 15
 Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly Gly Leu Ser Gly Phe
 20 25 30
 Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser Arg Ile Gly Leu Phe
 35 40 45
 Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro
 50 55 60
 Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
 65 70 75 80
 Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
 85 90 95

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln
 100 105 110
 Gly His Ile Arg Glu Leu Glu Glu Val Gln Leu Leu Lys Asn Leu
 115 120 125
 Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp
 130 135 140
 Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser
 145 150 155 160
 Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr
 165 170 175
 Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile
 180 185 190
 Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly
 195 200 205
 Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu
 210 215 220
 Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met
 225 230 235 240
 Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile
 245 250 255
 Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro
 260 265 270
 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg
 275 280 285
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys
 290 295 300
 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser
 305 310 315 320
 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu
 325 330 335
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
 340 345 350
 Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg
 355 360 365
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu
 370 375 380
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
 405 410 415
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr
 420 425 430
 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp
 435 440 445
 Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met Lys Ser Lys Ser Asn
 450 455 460
 Leu Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr Gly Val Pro Cys Asp
 465 470 475 480
 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp
 485 490 495
 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys
 500 505 510
 Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu Leu Glu Glu Phe His
 515 520 525
 Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala Leu Gly Asp Thr Asn
 530 535 540
 Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser Lys Thr Pro Lys Arg
 545 550 555 560
 Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp Ala Met Pro Ser Pro
 565 570 575
 Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser Arg Val Met Gln Ser
 580 585 590
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn
 595 600 605
 Asn Ser Arg Cys Phe Ser Glu Ile Arg Arg Lys Trp Glu Glu Glu Leu
 610 615 620
 Tyr Glu Glu Leu Glu Arg His Arg Glu Asn Leu Arg His Ala Gly Ala
 625 630 635 640
 Gly Gly Lys Thr Pro Leu Ser Gly His Lys Gly
 645 650

<210> 35
 <211> 1736
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS

<222> (1) .. (1605)

<400> 35

atg ccc cct cct aag atg ctt cca cca acg gca agg gat tca gta gca	48
Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala	
1 5 10 15	
ggg aca ggg ggt agt cca cca cct cca cct cca cca cca gct cgg tgg	96
Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp	
20 25 30	
agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
50 55 60	
ccc cct cct cgt cag cct cca cgt cct cca aca gca ccg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
65 70 75 80	
atg ggc aga gtg atg tgc agt ccg ccg ata cca cta tcg ccg agt aga	288
Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
85 90 95	
cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc ccg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser 225 230 235 240			720
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggc Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr 435 440 445			1344

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
 500 505 510
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
 515 520 525
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
 Gly Arg Arg Trp Arg Glu
 530 535
 tggaccggtt tagggcagtt gacggtaggg gttgcctgac cagccttgac gctcgacagc 1695
 taaaaaaaaac caacaaaaaaaa aaaaaaaaaaac aaaaaaaaaa a 1736

<210> 36
 <211> 534
 <212> PRT
 <213> Arabidopsis thaliana

<400> 36
 Met Pro Pro Pro Lys Met Leu Pro Pro Thr Ala Arg Asp Ser Val Ala
 1 5 10 15
 Gly Thr Gly Gly Ser Pro Pro Pro Pro Pro Pro Pro Ala Arg Trp
 20 25 30
 Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro
 35 40 45
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
 50 55 60
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
 65 70 75 80
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
 85 90 95
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
 115 120 125
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
 130 135 140
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
 145 150 155 160
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
 165 170 175
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
 180 185 190
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
 195 200 205
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
 210 215 220
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
 225 230 235 240
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
 245 250 255
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
 260 265 270
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
 275 280 285
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
 290 295 300
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
 305 310 315 320
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
 325 330 335
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
 340 345 350
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
 355 360 365
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
 370 375 380
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
 385 390 395 400
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
420 425 430

Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
435 440 445

Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
450 455 460

Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
465 470 475 480

Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
485 490 495

Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
500 505 510

Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
515 520 525

Gly Arg Arg Trp Arg Glu
530

<210> 37
<211> 508
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (18) .. (77)

<220>
<221> CDS
<222> (156) .. (314)

<220>
<221> CDS
<222> (374) .. (493)

<400> 37
gaagaaaatc tatcatc atg caa gtg gct gac ata tcc tta cag ggc gat 50
Met Gln Val Ala Asp Ile Ser Leu Gln Gly Asp
1 5 10

gct aag aag ggt gcc aac ctc ttc aag gtacgaacag agcaaagatg 97
Ala Lys Lys Gly Ala Asn Leu Phe Lys
15 20

ccgctgaaaa ttctcagggc gcattctatc ccgcagaact tttctgacca cttttag 155

acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203
Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
25 30 35

att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
 Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
 40 45 50

gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
 Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
 55 60 65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
 Lys Asp Asp Thr Leu
 70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
 Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
 75 80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
 Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
 85 90 95 100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
 Asn Asp Leu Ile Thr Phe Leu Glu Glu Thr Lys
 105 110

acccc 508

<210> 38
 <211> 112
 <212> PRT
 <213> Arabidopsis thaliana

<400> 38
 Met Gln Val Ala Asp Ile Ser Leu Gln Gly Asp Ala Lys Lys Gly Ala
 1 5 10 15

Asn Leu Phe Lys Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly
 20 25 30

Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
 35 40 45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
 50 55 60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
 65 70 75 80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
 85 90 95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
 100 105 110

<210> 39
 <211> 5156
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(609)

<220>
 <221> CDS
 <222> (686)..(841)

<220>
 <221> CDS
 <222> (933)..(1040)

<220>
 <221> CDS
 <222> (1130)..(1240)

<220>
 <221> CDS
 <222> (1341)..(2729)

<220>
 <221> CDS
 <222> (2772)..(2984)

<220>
 <221> CDS
 <222> (4112)..(4200)

<220>
 <221> CDS
 <222> (4241)..(4332)

<220>
 <221> CDS
 <222> (4478)..(4521)

<220>
 <221> CDS
 <222> (5088)..(5156)

<400> 39
 atg gca ccg aca cca tct tct tca aga tca aat caa act caa tac acc 48
 Met Ala Pro Thr Pro Ser Ser Ser Arg Ser Asn Gln Thr Gln Tyr Thr
 1 5 10 15

tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
 20 25 30

acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
 35 40 45

gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
 Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
 50 55 60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
 Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
 65 70 75 80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
 Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
 85 90 95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
 Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
 100 105 110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
 Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
 115 120 125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
 Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
 130 135 140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
 Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
 145 150 155 160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
 Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
 165 170 175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
 Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
 180 185 190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtctt ttgattgata 629
 Gly Ile Glu Trp Pro Lys Gly Ala Ser Thr Lys
 195 200

acttttagtat acattgaatt ggctttaag gtgtgtactt tggtgttttg ttacag gtg 688
 Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736
 Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
 205 210 215 220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
 Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
 225 230 235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
 Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
 240 245 250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881

His Cys Ile
255

atgcagctta tctctgtttt aacttactag tgtgggtgtt tctttttgta g atc ata 938
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
260 265 270

ggt tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144
Thr Ala Lys Ile Asn
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtgtt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355
Asp Ser Phe Glu Asp
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
ttt gtt gag atg gag aga agg aga atg gag gaa agg ata gtt cag cag	1835
Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
480 485 490	
caa gag gaa ctg gag atg atg agg aga cgg tta gag gaa atc gag gtt	1883
Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
495 500 505	
gag ttc cgc cgc tca aat gga gga agt gtt gat gaa act agt ggg ttt	1931
Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
510 515 520 525	
gcc aaa aga ctc agg agt ctt tac tct gat gat gat cct ggt atg gtg	1979
Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
aag tca atg gac ctt gac atg ggt gat cca gaa cct gtc aag caa gtg	2027
Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
tgg gga gct gtt tca cac caa tca agc aac act att agt agc aac ttc	2075
Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
aac tgc ttc aac ggt gca gat gac aag gaa tca gcc tcg tct aga agg	2315
Asn Cys Phe Asn Gly Ala Asp Asp Lys Glu Ser Ala Ser Ser Arg Arg	

640	645	650	
ttg aga att caa aac att ttc acc ctt tgt ggc aat cag aga gag ctg Leu Arg Ile Gln Asn Ile Phe Thr Leu Cys Gly Asn Gln Arg Glu Leu 655 660 665			2363
tct caa cac agt gga cag gag gag gat caa gcc aat att gca tca cct Ser Gln His Ser Gly Gln Glu Glu Asp Gln Ala Asn Ile Ala Ser Pro 670 675 680 685			2411
gat aag aaa gac aat cag ttc ttt tct att acg aat aag gcc gaa gca Asp Lys Lys Asp Asn Gln Phe Phe Ser Ile Thr Asn Lys Ala Glu Ala 690 695 700			2459
cta gca gta gaa gaa gca aag gaa aac aat atc tca gtc gat caa agg Leu Ala Val Glu Glu Ala Lys Glu Asn Asn Ile Ser Val Asp Gln Arg 705 710 715			2507
gaa aac ggt cag cta gat atc tat gtt aaa tgg gaa aca gct gct gat Glu Asn Gly Gln Leu Asp Ile Tyr Val Lys Trp Glu Thr Ala Ala Asp 720 725 730			2555
aac cct cga aag ctc ata aca aca ctg aga gtt aca aag gat gca aca Asn Pro Arg Lys Leu Ile Thr Thr Leu Arg Val Thr Lys Asp Ala Thr 735 740 745			2603
cta gct gac ttg agg aag ctt att gag atc tac ctt gga tct gat aat Leu Ala Asp Leu Arg Lys Leu Ile Glu Ile Tyr Leu Gly Ser Asp Asn 750 755 760 765			2651
cag gct ttt acc ttt ctc aag ctc ggg gta ata aac ttg aac caa caa Gln Ala Phe Thr Phe Leu Lys Leu Gly Val Ile Asn Leu Asn Gln Gln 770 775 780			2699
gca caa aaa gct ttt cat ttt tat ctg ttt gttatgctct gacctaagt Ala Gln Lys Ala Phe His Phe Tyr Leu Phe 785 790			2749
gcagttatatt caatgtatga ag gaa cca tgt gga gct caa gtg gca aag gag Glu Pro Cys Gly Ala Gln Val Ala Lys Glu 795 800			2801
aaa gaa tca aca gtt caa gct acg agc cta cct ctc tgc aac gga cac Lys Glu Ser Thr Val Gln Ala Thr Ser Leu Pro Leu Cys Asn Gly His 805 810 815			2849
gca tac ctc gcc act ttg aga cca gga aag agc tca caa cat aaa agt Ala Tyr Leu Ala Thr Leu Arg Pro Gly Lys Ser Ser Gln His Lys Ser 820 825 830			2897
ctt caa cct gca agc cca ctt cca ctt aat ccc ata gaa aac atg atg Leu Gln Pro Ala Ser Pro Leu Pro Leu Asn Pro Ile Glu Asn Met Met 835 840 845			2945
gaa gtt acc ccc atc tca aaa gtg aca ccg aac cat caa gttgatgaat Glu Val Thr Pro Ile Ser Lys Val Thr Pro Asn His Gln 850 855 860			2994

```

tttcatcacc caatctcgta gctcatctca gtcactcc attcatcact ctcagaagac 3054
attagtcgct atgtcttggt ttctctattc ttcttttggt tgtccaaagg tagcttttga 3114
aagatgtagc agcctttgtc tatttctctg tgttgagaaa aaaaaaactc ttatgtacga 3174
ccacttttgt agctatatat atgttctacg atgtttcagc agagtgggtg ttatcagaac 3234
gtataactgg tgtttcccaa aggatgctta gttctactta taacatatac ataagtagag 3294
agaatgctgc agccacatag agctacttct tacctctctc tgtcattgta acatatggac 3354
aaattccaaa agccctattc aattccaacc ccaatatctt tatgatcatc atcataacgt 3414
gaacacaaaa aacaagggca aaaatttcaa aggtctttaa aaataacaat atcccggaag 3474
caaagattac ctgcaactgc aagggaagc caagccctat tatagaaaag caacttcatt 3534
agttaagccc tatctctcaa tatgctcaca tgcattgatt gaccaaagt cttcttttat 3594
ctacaggtac tcagtcactt tcttagttac aactagatt aactcaattc ttctgcaacc 3654
tcattatctc caaagtaaaa gaccactggt attgatggtt ttatggataa tatatgatga 3714
ttcatcttta ttacattagc tgaatacaga acaacaacca attaatcaa ttattttgaa 3774
agatgtatgt agcctgtcta tttctcggtg ttgagaaaaa aaacgctatg tacgaccact 3834
ttcagcagtc aaagtgagtg actagagcca tcagcatgga gtgtttttca agttgtacaa 3894
caagatttgt caacaaagtc taaaactttc ttttattcga ccataaatg actgactagg 3954
cacgttggtt ttcgatatac agtttaaaag gttggagaag atgactagat gagataggtt 4014
ttcatatttt acttccacat cgaagtttta gagaacagaa agaggagaaa attgaagtac 4074
acatgagaca agttacactt taaagcttta ttaacag att ctt tta aaa aca gag 4129
                                Ile Leu Leu Lys Thr Glu
                                865
act gag aga ttg gga gag gca gat tac att aac tct ctt tct ctc tct 4177
Thr Glu Arg Leu Gly Glu Ala Asp Tyr Ile Asn Ser Leu Ser Leu Ser
870                                875                                880
cac ttt ctc atc ttg ttc cca ag gttaaaaaac aattcgagga catgtctttc 4230
His Phe Leu Ile Leu Phe Pro Ar
885                                890
ctattttcag a gga gag agc cat cag cac cga atg ttg tct ttt cac tct 4280
g Gly Glu Ser His Gln His Arg Met Leu Ser Phe His Ser
895                                900                                905
cat caa act tct cct tcc cta tct tca ttt cct ctt ctt tcc aga gcc 4328
His Gln Thr Ser Pro Ser Leu Ser Ser Phe Pro Leu Leu Ser Arg Ala
910                                915                                920

```

gat g gtaaggagct cgaagtttct aatggcatcc tcatgcccag gccttgctgc 4382
Asp A

agctgcagat tcatagctct gtggaacccg ttgggttggt gcatgacgtg aaccacttga 4442

aaatagtcgg cttgagtggg tctcgcttgg ttcag ct. gat gag cca ggt ctg gtg 4497
la Asp Glu Pro Gly Leu Val
925

ctt gat atc aca cct ctc ttt gag gtacttccat ttcgagactc gtgctgcaaa 4551
Leu Asp Ile Thr Pro Leu Phe Glu
930 935

tgaagccagc aaatcaaaac acacaaactt tctcatgttc tgattcccta cttattctga 4611

gaattacttt ggatcattac aacaagagaa ataacaacac aaactaacca cttccttggc 4671

agaagagggt atatcatcag aagatctgtg tctagagcga tcaccaagag cgccttggct 4731

tgaacatttt cgtctggtga atgcctcaat tgcacctgta aatcttcttc gcaggctcctg 4791

tccgactaaa cagaataggg aaagaagttc tcagtttgag atcttccact attcaacaat 4851

ttaattaaat ctctggacac aaattcaaaa tcttctaagg gaaacaacat atgaatgtta 4911

atatctgaag ggtcaagtga gatagtgcac gtttttcagc acccaaaatt gtcaacactg 4971

tctcataaat ttacaactta aaataaactt tttgatatat ctctttgtat tcgtccctcc 5031

aatataagag acagagaaca tcaatgtacc tgtaggcttt tcagctcttt ctgcag gtg 5090
Val

gtc ctg gag ggt cca acg ctg gtc ttg gag ttg gct gtt gta aat gat 5138
Val Leu Glu Gly Pro Thr Leu Val Leu Glu Leu Ala Val Val Asn Asp
940 945 950

aga cac ata gca gga taa 5156
Arg His Ile Ala Gly
955 960

<210> 40

<211> 959

<212> PRT

<213> Arabidopsis thaliana

<400> 40

Met Ala Pro Thr Pro Ser Ser Ser Arg Ser Asn Gln Thr Gln Tyr Thr
1 5 10 15

Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
20 25 30

Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
35 40 45

Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys

50 55 60
 Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
 65 70 75 80
 Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
 85 90 95
 Ser Glu Gln Glu Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
 100 105 110
 Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
 115 120 125
 Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
 130 135 140
 Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
 145 150 155 160
 Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
 165 170 175
 Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
 180 185 190
 Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys Val Arg Leu Glu Val
 195 200 205
 Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser Gly Thr Glu Ala
 210 215 220
 Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys Arg Arg Ile Val
 225 230 235 240
 Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser His Cys Ile Ile
 245 250 255
 Ile Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met
 260 265 270
 Ala Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala
 275 280 285
 Lys Met Gln Thr Ala Lys Ile Asn Gln Gly Asn Ile Ala Leu Lys Arg
 290 295 300
 Val Val Glu Ser Ile Ala Asn Gly Asp Ser His Val Pro Phe Arg Asp
 305 310 315 320
 Ser Lys Leu Thr Met Leu Leu Gln Asp Ser Phe Glu Asp Asp Lys Ser
 325 330 335
 Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys Glu Met His
 340 345 350
 Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys Cys Ile Val

355					360					365					
Arg	Gly	Ser	His	Thr	Pro	Asn	Lys	Asp	Lys	Tyr	Gly	Gly	Asp	Glu	Ser
370						375					380				
Ala	Ser	Ala	Val	Ile	Leu	Gly	Ser	Arg	Ile	Ala	Ala	Met	Asp	Glu	Phe
385					390					395					400
Ile	Ile	Lys	Leu	Gln	Ser	Glu	Lys	Lys	Gln	Lys	Glu	Lys	Glu	Arg	Asn
			405						410					415	
Glu	Ala	Gln	Lys	Gln	Leu	Lys	Lys	Lys	Glu	Glu	Glu	Val	Ala	Ala	Leu
			420					425					430		
Arg	Ser	Leu	Leu	Thr	Gln	Arg	Glu	Ala	Cys	Ala	Thr	Asn	Glu	Glu	Glu
		435					440					445			
Ile	Lys	Glu	Lys	Val	Asn	Glu	Arg	Thr	Gln	Leu	Leu	Lys	Ser	Glu	Leu
	450					455					460				
Asp	Lys	Lys	Leu	Glu	Glu	Cys	Arg	Arg	Met	Ala	Glu	Glu	Phe	Val	Glu
465						470					475				480
Met	Glu	Arg	Arg	Arg	Met	Glu	Glu	Arg	Ile	Val	Gln	Gln	Gln	Glu	Glu
			485						490					495	
Leu	Glu	Met	Met	Arg	Arg	Arg	Arg	Leu	Glu	Glu	Ile	Glu	Val	Glu	Phe
			500					505						510	Arg
Arg	Ser	Asn	Gly	Gly	Ser	Val	Asp	Glu	Thr	Ser	Gly	Phe	Ala	Lys	Arg
		515					520					525			
Leu	Arg	Ser	Leu	Tyr	Ser	Asp	Asp	Asp	Pro	Gly	Met	Val	Lys	Ser	Met
	530					535					540				
Asp	Leu	Asp	Met	Gly	Asp	Pro	Glu	Pro	Val	Lys	Gln	Val	Trp	Gly	Ala
545						550					555				560
Val	Ser	His	Gln	Ser	Ser	Asn	Thr	Ile	Ser	Ser	Asn	Phe	Thr	Asn	Leu
			565					570						575	
Leu	Gln	Pro	Lys	Pro	Ser	Glu	Asn	Met	Leu	Thr	Gln	Met	Tyr	Pro	Asp
			580					585					590		
Arg	Val	Cys	Leu	Ser	Thr	Val	Phe	Glu	Glu	Glu	Glu	Val	Glu	Glu	Glu
		595					600					605			
Glu	Glu	Lys	Val	Ile	Val	Glu	Asp	Lys	Ser	Ile	Cys	Leu	Ile	Thr	Thr
	610					615					620				
Pro	Met	Pro	Ser	Leu	Asn	Ser	Glu	Gly	Leu	Gly	Lys	Glu	Asn	Cys	Phe
	625					630			635					640	
Asn	Gly	Ala	Asp	Asp	Lys	Glu	Ser	Ala	Ser	Ser	Arg	Arg	Leu	Arg	Ile
			645						650					655	
Gln	Asn	Ile	Phe	Thr	Leu	Cys	Gly	Asn	Gln	Arg	Glu	Leu	Ser	Gln	His

86

<210> 41
 <211> 6960
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (147)..(327)

<220>
 <221> CDS
 <222> (405)..(796)

<220>
 <221> CDS
 <222> (1426)..(1500)

<220>
 <221> CDS
 <222> (3486)..(3638)

<220>
 <221> CDS
 <222> (3754)..(3864)

<220>
 <221> CDS
 <222> (4030)..(4096)

<220>
 <221> CDS
 <222> (4252)..(4523)

<220>
 <221> CDS
 <222> (4732)..(4834)

<220>
 <221> CDS
 <222> (6735)..(6907)

<400> 41
 cccaaaaagc ttgacctaac ggctatgttt tctttacttt caccataaat aagcacctct 60
 tgagggttgca aacacacaca cacacacaca ctcaattcaa aagagttagt aagaagttgg 120
 ggtttgatta acgttttgca tcggag atg ggt ttg gtc atg agg ttt gat ctt 173
 Met Gly Leu Val Met Arg Phe Asp Leu
 1 5
 tac ctt atg ttt gtg atg ttg atg ggt tta ggg ttt acg ata tca aat 221
 Tyr Leu Met Phe Val Met Leu Met Gly Leu Gly Phe Thr Ile Ser Asn
 10 15 20 25
 gga tac aag ttc tat gtt ggt ggg aaa gat ggt tgg gtc ccg act cct 269
 Gly Tyr Lys Phe Tyr Val Gly Gly Lys Asp Gly Trp Val Pro Thr Pro

30	35	40	
tcc gaa gat tat tct cat tgg tct cac cga aac cgg ttt caa gtc aac			317
Ser Glu Asp Tyr Ser His Trp Ser His Arg Asn Arg Phe Gln Val Asn			
45	50	55	
gac act ctt c gtaagtctat ttcctcttct ctactatata tacacaatgt			367
Asp Thr Leu H			
60			
gtcaatatta atgcatagta attttgattt ttacaag at ttt aag tac gcc aag			421
		is Phe Lys Tyr Ala Lys	
		65	
gga aaa gat tca gtg ttg gag gtg act gaa caa gag tac aac aca tgc			469
Gly Lys Asp Ser Val Leu Glu Val Thr Glu Gln Glu Tyr Asn Thr Cys			
70	75	80	
aac acg aca cac ccc ctg act tcc ctc tca gac gga gac tct ctc ttc			517
Asn Thr Thr His Pro Leu Thr Ser Leu Ser Asp Gly Asp Ser Leu Phe			
85	90	95	
cta ctt agc cac tca ggt tcc tac ttt ttc att agt ggc aac tct caa			565
Leu Leu Ser His Ser Gly Ser Tyr Phe Phe Ile Ser Gly Asn Ser Gln			
100	105	110	
aac tgt ctt aaa ggt cag aag cta gcc gtc aag gtc ttg tcc acc gtc			613
Asn Cys Leu Lys Gly Gln Lys Leu Ala Val Lys Val Leu Ser Thr Val			
115	120	125	130
cac cac agc cac tct cct cgt cat acc tct ccc tcc ccg tct ccg gtc			661
His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser Pro Val			
135	140	145	
cat cag gag ttg tct tcg ccg ggg cct tct cca gga gtg gaa cca tca			709
His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu Pro Ser			
150	155	160	
tct gat tca aac tct cgt gtt cca gct cca gga ccg gct aca gct ccc			757
Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr Ala Pro			
165	170	175	
aat tcg gcc ggt ttg gtt ggt ccg ggg atg gtg gtt ctt gtgattatga			806
Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu			
180	185	190	
taagttctct gttttgaggg gtttatatat tgtcgctagt cattaaattt gtgagggtat			866
taattactct accattgagt ttcataattta tgtgcctttt tatttgtatg tttgaagcat			926
cttgtaaccc atttttaatg tttccgctgt ctcggttttg ttcttactaa agaaaatatt			986
taagatgttt ttttgtattg attagatgcg aatgttttta ttttgtgttt taattatgat			1046
cacactaata tgaatatata cgacgaatat gtagagttca catagctcat gcaataaaac			1106
ttctccacac aaactaaaat cttgttgaaa catataaata gatcttatac acttttttga			1166

catataagaa tggtttgaac aatttaactt taatcaatat attaaaccgg tacaccgaaa 1226
tccaatagag agaatatgtc aaggagttaa caaaaaaaat atactaccgc cgtctgtggg 1286
gatcgaaccc acggcctcgt gggtaaaagc cacgcgctct accactgagc taagacggct 1346
atatgacaaa aaattttaat tatgttaatt attgtatggt tttgcagatc aaattaccaa 1406
tgaaatagtt ggtatttag gtt gtt aac tca atc ata aag ccg att gac tct 1458
Val Val Asn Ser Ile Ile Lys Pro Ile Asp Ser
195 200
ttt ttg ttg aag agc ttg cct ctt gtt gtg gat gtg gct gtt 1500
Phe Leu Leu Lys Ser Leu Pro Leu Val Val Asp Val Ala Val
205 210 215
gtaagactaa taccagccct tgggtcgaaa gttgaaagtt tgattctgga tctctaattgt 1560
ctctagtatg gacgctcctg tttggaagtc ttttgtttgg aatatgatat agattcataa 1620
aatgcggggt atctactacc atttgctatt gaccatcaaa aaaacaacaa agtctcttaa 1680
ctatcttaaa attttattag gagattttca tgcgactaga acaagatttt caagcagtgg 1740
atgataagac aaaactgata ggccaacaac ttgatgaaat gggcaatatt atgaaataat 1800
acacaagtat agcttccacc tccaaccacc taaggacctc taataaattt acccaccaaa 1860
ggtggtggga ctccgtcaca gagccgtgcc tcaaggcaaa agaaagaac attcgcctac 1920
gtcctcaaat ttttgaaaaa aacttaggag catatatattt tacaagataa ctttagtttc 1980
ataggtttta tattgacaaa tcacttacat ttacctaaat aataaaaata tagaattaaa 2040
aatagaaaaa tattcacaga ataaataaat aaaacagaac aaagcattat aaatttaggt 2100
taaagcattc gatatagaat tggttaaaaa aattaacttt gaatcttttg tcatatgaca 2160
atttatattt gtaaacactt ttacttctat tattataagc atctttgctt gtgaattggg 2220
gcaaatttca tttggccgcc tccggcaacc attgaccttg gcacggctct gctccgtcac 2280
ctcttatatt tgctgcaatg gcacagagaa gagaaattag ttgctgggtg tgatccctaa 2340
tatgtgctag ttcacatctt acatgtccaa atctaaatct catcccttct cctatcgcac 2400
ggacctgcaa gtgtagaaag caaaaacatc aacatatattt aataataatt acaaaacaca 2460
ttaggttctt aaacttatca aaactaatta cttcaaaaaa tatctttcta aaagttaata 2520
taccggaatt taatgcattt aaactagaat tttttttcta taaattaaat gtataataaa 2580
atccataaaa taaattttta taagctctta ctaattaaac ataagataaa acaatattat 2640
taatttctca acaatcaaat gtgtagagaa accaaaaaga taaaataaac tcggatgtca 2700

taggcccata atccagcctt ttctcaaagc ttaaaccgtaa cgggctcggc ccaaatttgg 2760
 tgtgttcata atcttcccca caaacctaa ttttgtttct tcagtagtac tgtagcttca 2820
 gatgcaactc ctcgaaaacc cgtagaaccg gcattgagcc aatcgtttac attctctgat 2880
 tcatatcctt agcgttttca gaaacaaaat ggtgggttgg aagaggaatt tgcagactgt 2940
 tattcgtcaa gttggtagaa gagtgaagaa cagtcacatt tctacagcaa attactcttc 3000
 ttctactcgg aatttagaat cccctttctc acaagggtga ctttttgatc atttccgaaa 3060
 tctagtgtgt ttcttagtgg gtctttcaaa gggcatgtgt tatctggtct tctgtttgt 3120
 gaattgtgtg tttgagttga gtttttttgc tgggtattat aggttacttg cagagctctc 3180
 tgagaccatc ctactctctc agaccactgt atcatcatct acaacaactg gtaatgcatt 3240
 tgaatcgaca tttcttttgt gttttactga gattggagtt tcttgtttcc tgatatagca 3300
 aatttgttgc tgcattgaaa aatcgaattt caaaatttgg gaagtgaagaa tgttgctagt 3360
 gggagactat atctgttate catgtgaatt aggcgaagag actcatcttt tggaactatg 3420
 cgtctctagt caacttaggg acctgtactt tagggtatga aatttcaatt tgggtatgtt 3480
 ttcag ggg atc tct acc tcg aga caa ttg cag gcg agt gaa gag cct gta 3530
 Gly Ile Ser Thr Ser Arg Gln Leu Ala Ser Glu Glu Pro Val
 220 225 230
 tca tca cct ttg tca tct cca gct ctg ttg ggt agt gga aaa gaa gaa 3578
 Ser Ser Pro Leu Ser Ser Pro Ala Leu Leu Gly Ser Gly Lys Glu Glu
 235 240 245
 gag cag aag att atc cca aag cgt cag aaa gtt cag gct gtc ctc aag 3626
 Glu Gln Lys Ile Ile Pro Lys Arg Gln Lys Val Gln Ala Val Leu Lys
 250 255 260
 tct ata aag cag gtgtcttctt taactcctag aacagtttta cttttcagat 3678
 Ser Ile Lys Gln
 265
 gatctgctcc atttcgttta atatttttcc atctcaatct agttatataa tgtgcccac 3738
 cttgcttgtt ttcag agt cct aag aag gtc aac ctg gtt gca gca cta gtc 3789
 Ser Pro Lys Lys Val Asn Leu Val Ala Ala Leu Val
 270 275
 cgt ggc atg cgt gtt gaa gat gct ttg atc caa ttg cag gtc aca gtc 3837
 Arg Gly Met Arg Val Glu Asp Ala Leu Ile Gln Leu Gln Val Thr Val
 280 285 290 295
 aaa cga gct gca caa act gtg tac cgg gtaatctctg agatccgagt 3884
 Lys Arg Ala Ala Gln Thr Val Tyr Arg
 300
 ttacaaacaa atcactgttg gatttcgagt gtctagtcta atctcctctc caggcatttg 3944

71:

tttatcagtt tgttccactt cttaatgcaa tttttggata ttaaaagaat aaatgaatga 4904
atatacatat gcattttggt tgttgagaat atttatttag tcatttattt aagaaattta 4964
tattttaatt ttttattatt aatatgatat ttgttttgtc actatgttac aacataattc 5024
aattttaata tcattataat tgatagtaat aataataaat aacagtcaca ggcccctacc 5084
atcatcccaa aatgattcat gcaatttagt catcaaatac atacaatctt atatacaaaa 5144
gaatcacaca gcatgtataa actaatagta tagaaattcg attaaaaaat actcccaggc 5204
tagttttttc accttccatg aagaatagaa tcataagttt ggaaggaatt agaataagaa 5264
gacgaattcc atacatcttg gaacgtggga tgttgttgtc tgcttccctc accagtttcc 5324
aacaagtaag agctcttcac tctctccaac aagcttattt ccttttcacc accatcctcc 5384
actaatctcc cttgttccaa tatctgcacc acttgtctca tcttcggacg cactctcgga 5444
tcaggatgca cacacaacag tctattctc agagccatct ccacttcctc gaccacgaac 5504
actccattcg cctttattct ctctctaaa ccatcaacca ctttgtcttt ctccattagt 5564
ccccatatcc attccactat cccttctctt ccttctctta ttggcctcct tccacacact 5624
acctccaaca caaacactcc aaagctatac acatcggttt gcgctgatgc tctccctgtc 5684
ttaaccaact caggcgccat ataaccgct gtccaacaa catgtgtcgt gctaacctac 5744
tctttactag tgttctgcaa cttagccaac ccaaatcac ctaccctcg gttcatatcc 5804
ttgtcaagca acacattgct tgactttata tctctatgta acacctttgt cteccacct 5864
tcgtgtagat acaacatccc tgaggctagg tctcttatca ctctcattct ttctcccaa 5924
ttcaacatct cgttacaatc aaatatccgc ttatcgacac ttccattctc catatactcg 5984
taaatcaata tcagactctc tctcctttc ttagaccaac cttttagtcc aactatattc 6044
ttgtgtctca acctccctaa gctcgagacc tcagctaaga actcactcgt cgcgccaacg 6104
ctctctcgag gactcatcat tattctctta accgcaactt ctttaccttc caacactccc 6164
ctgtacactt tagaattccc tccgtatccg atcatgttct catcggaata cccttttgtt 6224
gcttccaaaa catctttgta ttgcactctg tgaggccaat actctgtttc ccaatcttcc 6284
acgtctcctt ctagtctctg ccttcgacgc cttacaacgt agaaacagag gagcccaata 6344
acagagacta acaacacaac accactagag accccagcaa tgaagccttt agacttcaaa 6404
acagagtcac ctgacaattt aaacgaaggt agattcctag tgatcaaagc atcaccaatg 6464
gagaaattgg agttactaaa actccatgag agaatcctat ggctctgcac tagttgtcct 6524

Thr Val His His Ser His Ser Pro Arg His Thr Ser Pro Ser Pro Ser
 130 135 140
 Pro Val His Gln Glu Leu Ser Ser Pro Gly Pro Ser Pro Gly Val Glu
 145 150 155 160
 Pro Ser Ser Asp Ser Asn Ser Arg Val Pro Ala Pro Gly Pro Ala Thr
 165 170 175
 Ala Pro Asn Ser Ala Gly Leu Val Gly Pro Gly Met Val Val Leu Val
 180 185 190
 Val Asn Ser Ile Ile Lys Pro Ile Asp Ser Phe Leu Leu Lys Ser Leu
 195 200 205
 Pro Leu Val Val Asp Val Ala Val Gly Ile Ser Thr Ser Arg Gln Leu
 210 215 220
 Gln Ala Ser Glu Glu Pro Val Ser Ser Pro Leu Ser Ser Pro Ala Leu
 225 230 235 240
 Leu Gly Ser Gly Lys Glu Glu Glu Gln Lys Ile Ile Pro Lys Arg Gln
 245 250 255
 Lys Val Gln Ala Val Leu Lys Ser Ile Lys Gln Ser Pro Lys Lys Val
 260 265 270
 Asn Leu Val Ala Ala Leu Val Arg Gly Met Arg Val Glu Asp Ala Leu
 275 280 285
 Ile Gln Leu Gln Val Thr Val Lys Arg Ala Ala Gln Thr Val Tyr Arg
 290 295 300
 Val Ile His Ala Ala Arg Ala Asn Ala Thr His Asn His Gly Leu Asp
 305 310 315 320
 Pro Asp Arg Leu Leu Val Ala Glu Ala Phe Val Gly Lys Gly Leu Phe
 325 330 335
 Gly Lys Lys Val Ala Tyr His Ala Lys Gly Arg Ser Gly Ile Ile Ser
 340 345 350
 Ile Pro Arg Cys Arg Leu Thr Val Ile Val Arg Glu Thr Thr Pro Glu
 355 360 365
 Glu Glu Ala Glu Ile Ala Arg Leu Lys Val His Asn Phe Lys Lys Lys
 370 375 380
 Ser Lys Arg Glu Arg Gln Leu Val Pro His Lys Leu Ile Glu Thr Ser
 385 390 395 400
 Pro Ile Trp Asn Arg Arg Gly Thr Lys Ala Asn His Arg Ser Ser Glu
 405 410 415
 Leu Val Leu Thr Ile Ile Leu Asp Val Thr Cys Val Gly Asn Met Glu
 420 425 430

Lys Asn Arg Leu Asp Asn Leu Thr Asn Gln Asn Asn Ile Tyr His His
 435 440 445
 Asn Pro Glu Glu Thr Cys Ser Phe Arg Cys Asn Gly Ser Glu Arg Ile
 450 455 460
 Asp Val Asp Ala Asp Val Val Val Val Asp Val Val Glu Leu Leu Val
 465 470 475 480
 Ser Glu Asn Ile Glu Phe Asn Gly Glu Asp Ser Ala Ile Gly Val Thr
 485 490 495
 Val Ile Gly Glu Val Glu Glu Ala Glu Met Leu Arg
 500 505

<210> 43
 <211> 729
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (26)..(718)

<400> 43

ctgcggcacc ggcgtcggag ttgcg atg ttc gcc aac aag ttc ccg ggc gtc 52
 Met Phe Ala Asn Lys Phe Pro Gly Val
 1 5
 tac gca gcc act tgt ctc tcc gtc gaa gac gcc gtc aac gct cga tca 100
 Tyr Ala Ala Thr Cys Leu Ser Val Glu Asp Ala Val Asn Ala Arg Ser
 10 15 20 25
 ata agc aat tgc aat gtc ctc gca ttc tcc ggc atc aaa aca tcc ccg 148
 Ile Ser Asn Cys Asn Val Leu Ala Phe Ser Gly Ile Lys Thr Ser Pro
 30 35 40
 gaa acc gcc ttg gaa atc ttc gac gct tgg atc aaa act cct ttc aaa 196
 Glu Thr Ala Leu Glu Ile Phe Asp Ala Trp Ile Lys Thr Pro Phe Lys
 45 50 55
 tct cct tgt cct gcg tcc gga tcc gaa cca tgg agc tca gtt atc tct 244
 Ser Pro Cys Pro Ala Ser Gly Ser Glu Pro Trp Ser Ser Val Ile Ser
 60 65 70
 tcc ttc ctc gac aat tct ctc tcc gag atg tct cag att gga aag tca 292
 Ser Phe Leu Asp Asn Ser Leu Ser Glu Met Ser Gln Ile Gly Lys Ser
 75 80 85
 acc gcc ggc gat tca aca acc aag aag atc gat gaa aca acc gcg tct 340
 Thr Ala Gly Asp Ser Thr Thr Lys Lys Ile Asp Glu Thr Thr Ala Ser
 90 95 100 105
 tgc gta att tgc tgc ttg gcg aag aac aga gag ttc act cca gtg gac 388

Cys Val Ile Cys Cys Leu Ala Lys Asn Arg Glu Phe Thr Pro Val Asp
 110 115 120
 atc atg ccg gga ggc tcg atg aag atc gtt aga gag acg ccg acg tcg 436
 Ile Met Pro Gly Gly Ser Met Lys Ile Val Arg Glu Thr Pro Thr Ser
 125 130 135
 gcg att gta aga ttc aaa gcg gga agt gtg gaa ccg gcg cat cac cac 484
 Ala Ile Val Arg Phe Lys Ala Gly Ser Val Glu Pro Ala His His His
 140 145 150
 aca ttc ggc cat gac ctt gta gtc ata aag gga aag aaa agt gtg tgg 532
 Thr Phe Gly His Asp Leu Val Val Ile Lys Gly Lys Lys Ser Val Trp
 155 160 165
 aat ctg agc aag aag gag aga gct gat ctc gtt gac ggc gat tac cta 580
 Asn Leu Ser Lys Lys Glu Arg Ala Asp Leu Val Asp Gly Asp Tyr Leu
 170 175 180 185
 ttc act ccc gcc ggt gat gtt cac cga gtc aaa tat cac gaa gac act 628
 Phe Thr Pro Ala Gly Asp Val His Arg Val Lys Tyr His Glu Asp Thr
 190 195 200
 gag ttc ttc atc act tgg gat ggc cat tgg gac ata ttc ctt gac gaa 676
 Glu Phe Phe Ile Thr Trp Asp Gly His Trp Asp Ile Phe Leu Asp Glu
 205 210 215
 gac ctc gaa act gca aag aaa gcc atc gaa gaa gaa gct tga 718
 Asp Leu Glu Thr Ala Lys Lys Ala Ile Glu Glu Glu Ala
 220 225 230
 aggtgtaaac t 729

<210> 44
 <211> 230
 <212> PRT
 <213> Arabidopsis thaliana

<400> 44
 Met Phe Ala Asn Lys Phe Pro Gly Val Tyr Ala Ala Thr Cys Leu Ser
 1 5 10 15
 Val Glu Asp Ala Val Asn Ala Arg Ser Ile Ser Asn Cys Asn Val Leu
 20 25 30
 Ala Phe Ser Gly Ile Lys Thr Ser Pro Glu Thr Ala Leu Glu Ile Phe
 35 40 45
 Asp Ala Trp Ile Lys Thr Pro Phe Lys Ser Pro Cys Pro Ala Ser Gly
 50 55 60
 Ser Glu Pro Trp Ser Ser Val Ile Ser Ser Phe Leu Asp Asn Ser Leu
 65 70 75 80
 Ser Glu Met Ser Gln Ile Gly Lys Ser Thr Ala Gly Asp Ser Thr Thr
 85 90 95

Lys Lys Ile Asp Glu Thr Thr Ala Ser Cys Val Ile Cys Cys Leu Ala
100 105 110

Lys Asn Arg Glu Phe Thr Pro Val Asp Ile Met Pro Gly Gly Ser Met
115 120 125

Lys Ile Val Arg Glu Thr Pro Thr Ser Ala Ile Val Arg Phe Lys Ala
130 135 140

Gly Ser Val Glu Pro Ala His His His Thr Phe Gly His Asp Leu Val
145 150 155 160

Val Ile Lys Gly Lys Lys Ser Val Trp Asn Leu Ser Lys Lys Glu Arg
165 170 175

Ala Asp Leu Val Asp Gly Asp Tyr Leu Phe Thr Pro Ala Gly Asp Val
180 185 190

His Arg Val Lys Tyr His Glu Asp Thr Glu Phe Phe Ile Thr Trp Asp
195 200 205

Gly His Trp Asp Ile Phe Leu Asp Glu Asp Leu Glu Thr Ala Lys Lys
210 215 220

Ala Ile Glu Glu Glu Ala
225 230

<210> 45

<211> 1203

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (12)..(1193)

<400> 45

aggaaagaga a atg act ata agg aac caa cga ttc tct ctt ctt aaa caa 50
Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln
1 5 10

cct ata tcc tcc aca ctt aat cag cat tta gta gat tat cca acc ccg 98
Pro Ile Ser Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro
15 20 25

agc aat ctt agt tat tgg tgg ggg ttc ggt ccg tta gct ggt att tgt 146
Ser Asn Leu Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys
30 35 40 45

tta gtc att cag ata gtg act ggc gtt ttt tta gct atg cat tac aca 194
Leu Val Ile Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr
50 55 60

cct cat gtg gat tta gct ttc aac agc gta gaa cac att atg aga gat 242

Pro His Val Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp	
65 70 75	
ggt gaa ggg ggc tgg ttg ctc cgt tat atg cat gct aat ggg gca agt	290
Val Glu Gly Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser	
80 85 90	
atg ttt ctt att gtg gtt tac ctt cat att ttt cgt ggt cta tat cat	338
Met Phe Leu Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His	
95 100 105	
gcg agt tat agc agt cct agg gaa ttt gtt tgg tgt ctt gga gtt gta	386
Ala Ser Tyr Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val	
110 115 120 125	
atc ttc cta tta atg att gtg aca gct ttt ata gga tat gta cta cct	434
Ile Phe Leu Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro	
130 135 140	
tgg ggt cag atg agc ttt tgg gga gct aca gta att aca agc tta gct	482
Trp Gly Gln Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala	
145 150 155	
agc gcc ata cct gta gta gga gat acc ata gtg act tgg ctt tgg ggt	530
Ser Ala Ile Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly	
160 165 170	
ggt ttc tcc gtg gac aat gcc acc tta aat cgt ttt ttt agt ctt cat	578
Gly Phe Ser Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His	
175 180 185	
cat tta ctc ccc ttt att tta gta ggc gcc agt ctt ctt cat ctg gcc	626
His Leu Leu Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala	
190 195 200 205	
gca ttg cat caa tat gga tca aat aat cca ttg ggt gta cat tct gag	674
Ala Leu His Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu	
210 215 220	
atg gat aaa ata gct ttt tac cct tat ttt tat gtc aag gat cta gtt	722
Met Asp Lys Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val	
225 230 235	
ggt tgg gta gct ttt gct atc ttt ttt tct att tgg att ttt tat gct	770
Gly Trp Val Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala	
240 245 250	
cct aat gtt ttg gga cat ccc gac aat tat ata cct gct aat ccg atg	818
Pro Asn Val Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met	
255 260 265	
tcc acc ccg cct cat att gtg ccg gaa tgg tat ttc cta ccg atc cat	866
Ser Thr Pro Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His	
270 275 280 285	
gcc att ctt cgt agt ata cct gac aaa gcg gga ggt gta gcc gca ata	914
Ala Ile Leu Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile	

290	295	300	
gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg			962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met			
305	310	315	
tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct			1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga			1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtga			1203
Ile Pro Asn Ser Tyr Thr Asp Glu Thr Asp His Thr			
385	390		

<210> 46

<211> 393

<212> PRT

<213> Arabidopsis thaliana

<400> 46

Met Thr Ile Arg Asn Gln Arg Phe Ser Leu Leu Lys Gln Pro Ile Ser
1 5 10 15

Ser Thr Leu Asn Gln His Leu Val Asp Tyr Pro Thr Pro Ser Asn Leu
20 25 30

Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile
35 40 45

Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val
50 55 60

Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly
65 70 75 80

Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu
85 90 95

Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr
100 105 110

Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu
115 120 125

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
 130 135 140
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
 145 150 155 160
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
 165 170 175
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
 180 185 190
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
 195 200 205
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
 210 215 220
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
 225 230 235 240
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
 245 250 255
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
 260 265 270
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
 275 280 285
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
 290 295 300
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
 305 310 315 320
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
 325 330 335
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
 340 345 350
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
 355 360 365
 Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly Ile Pro Asn
 370 375 380
 Ser Tyr Thr Asp Glu Thr Asp His Thr
 385 390

<210> 47

<211> 1194

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)...(1194)

<400> 47

atg	aga	aaa	gtt	tct	tcc	gta	att	tct	gtc	gtt	gat	ccc	gtt	att	ttc	48
Met	Arg	Lys	Val	Ser	Ser	Val	Ile	Ser	Val	Val	Asp	Pro	Val	Ile	Phe	
1				5					10					15		
cga	gga	aat	tac	gca	gct	aca	ctc	gat	gtg	tcg	tat	ccg	gta	ttc	ccg	96
Arg	Gly	Asn	Tyr	Ala	Ala	Thr	Leu	Asp	Val	Ser	Tyr	Pro	Val	Phe	Pro	
			20					25					30			
caa	aat	aaa	gat	ggc	cgt	gca	ctt	cag	aaa	gtt	ctc	gga	acc	att	cgt	144
Gln	Asn	Lys	Asp	Gly	Arg	Ala	Leu	Gln	Lys	Val	Leu	Gly	Thr	Ile	Arg	
		35				40					45					
aac	gga	gat	ttg	gct	gtt	tcg	gct	cct	aaa	aca	agt	ctt	agg	gca	ggt	192
Asn	Gly	Asp	Leu	Ala	Val	Ser	Ala	Pro	Lys	Thr	Ser	Leu	Arg	Ala	Gly	
	50					55					60					
att	ttc	ggt	gaa	ggt	tcc	agc	ttg	gtc	gat	cag	atg	ccc	tgt	aaa	gtt	240
Ile	Phe	Gly	Glu	Gly	Ser	Ser	Leu	Val	Asp	Gln	Met	Pro	Cys	Lys	Val	
65					70				75					80		
tac	gtg	gcg	ttc	cac	aaa	gaa	tca	tac	tgc	tcg	ctt	acc	ggg	cta	agc	288
Tyr	Val	Ala	Phe	His	Lys	Glu	Ser	Tyr	Cys	Ser	Leu	Thr	Gly	Leu	Ser	
				85					90					95		
aaa	cgc	gga	gtc	gca	ata	aac	gaa	gca	agt	ctt	tcc	ctg	gtc	gga	atc	336
Lys	Arg	Gly	Val	Ala	Ile	Asn	Glu	Ala	Ser	Leu	Ser	Leu	Val	Gly	Ile	
			100					105					110			
act	aaa	gtt	aga	gcc	ccc	gtc	gga	aat	acc	gtt	gga	gcg	gaa	gca	acc	384
Thr	Lys	Val	Arg	Ala	Pro	Val	Gly	Asn	Thr	Val	Gly	Ala	Glu	Ala	Thr	
		115				120						125				
gta	tac	ata	ggt	agt	cca	aaa	cct	tat	aca	gag	tgt	agt	act	cca	aat	432
Val	Tyr	Ile	Gly	Ser	Pro	Lys	Pro	Tyr	Thr	Glu	Cys	Ser	Thr	Pro	Asn	
	130					135					140					
aaa	atg	tat	gcg	gtt	gca	gct	ggt	ttc	aag	gtg	gca	agt	ttc	gcc	gct	480
Lys	Met	Tyr	Ala	Val	Ala	Ala	Gly	Phe	Lys	Val	Ala	Ser	Phe	Ala	Ala	
145					150				155					160		
agt	acg	tgc	gta	cgt	ccg	cct	gca	cgt	gca	cgt	cgt	acg	ctg	acc	gtg	528
Ser	Thr	Cys	Val	Arg	Pro	Pro	Ala	Arg	Ala	Arg	Arg	Thr	Leu	Thr	Val	
				165				170						175		
acg	tcg	acc	gtg	acg	ctg	tct	atg	gca	act	ggt	aaa	tgc	gta	aat	aca	576
Thr	Ser	Thr	Val	Thr	Leu	Ser	Met	Ala	Thr	Gly	Lys	Cys	Val	Asn	Thr	
			180					185					190			
gga	aac	gaa	cca	gta	tct	aaa	cct	aca	gga	gta	cgt	atg	atg	tta	att	624
Gly	Asn	Glu	Pro	Val	Ser	Lys	Pro	Thr	Gly	Val	Arg	Met	Met	Leu	Ile	
		195					200					205				


```

cct ctc gat gct act ctc att aaa gta tgg act ggg gaa gta aaa aaa 672
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys
210 215 220

gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
290 295 300

gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggt gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
370 375 380

cgt acg acg atg atc gcc gtt ggt gaa agc aac gca aac tga 1194
Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
385 390 395

```

<210> 48

<211> 397

<212> PRT

<213> Arabidopsis thaliana

<400> 48

Met Arg Lys Val Ser Ser Val Ile Ser Val Val Asp Pro Val Ile Phe

1	5	10	15
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro	20	25	30
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg	35	40	45
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly	50	55	60
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val	65	70	75
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser	85	90	95
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile	100	105	110
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr	115	120	125
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn	130	135	140
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala	145	150	155
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val	165	170	175
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr	180	185	190
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile	195	200	205
Pro Leu Asp Ala Thr Leu Ile Lys Val Trp Thr Gly Glu Val Lys Lys	210	215	220
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu	225	230	235
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala	245	250	255
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg	260	265	270
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu	275	280	285
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu	290	295	300
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser			

305 310 315 320
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
 325 330 335
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
 340 345 350
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
 355 360 365
 Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
 370 375 380
 Arg Thr Thr Met Ile Ala Val Gly Glu Ser Asn Ala Asn
 385 390 395

<210> 49
 <211> 611
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (5)..(601)

<400> 49
 gaaa atg atc gta ctt tct gtt ggt tcc gct tct tca tct ccg atc gtc 49
 Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val
 1 5 10 15
 gtc gtc ttt tcc gtc gcg ctt ctt ctg ttc tac ttc tct gaa act tct 97
 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
 20 25 30
 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
 35 40 45
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
 50 55 60
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
 65 70 75
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
 80 85 90 95
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
 100 105 110

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
 115 120 125

ttt gcc aac agt aca att cat att ccg atc aat gat gct cat cag gtc 433
 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
 130 135 140

aaa aac acc ggt cat gag gac ctg cag gtg ttg gtt atc ata tct cgg 481
 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
 145 150 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
 160 165 170 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
 180 185 190

gaa tca caa aaa gac gag ctt taa agcaaagtcc 611
 Glu Ser Gln Lys Asp Glu Leu
 195

<210> 50
 <211> 198
 <212> PRT
 <213> Arabidopsis thaliana

<400> 50
 Met Ile Val Leu Ser Val Gly Ser Ala Ser Ser Ser Pro Ile Val Val
 1 5 10 15

Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser Leu
 20 25 30

Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile Ser
 35 40 45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
 50 55 60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
 65 70 75 80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
 85 90 95

Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
 100 105 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
 115 120 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
 130 135 140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
 145 150 155 160

Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
 165 170 175

Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu
 180 185 190

Ser Gln Lys Asp Glu Leu
 195

<210> 51
 <211> 1398
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(1398)

<400> 51
 atg cct cgt cgt cgt acg tgc tgt cgg cgt gaa ttc ggt ccg aca cag 48
 Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
 1 5 10 15

cca tgt aga ggc gcg tca atc act gga tct cta cgt gac cgt cga ccg 96
 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
 20 25 30

acc gct atc ctt atc gga acc ctc acc gct tta ggc ggt gga gtt aga 144
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
 35 40 45

tgt ggc tct tgc ccc agt gtc gac cgt tgc gga cac gca agt gcc gcc 192
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60

ata gcg cgt gat agc tgt gcc gtg ttc gca tgg aag cga ggt acg cga 240
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80

caa gag tac tgg tgc tcg act gaa ccg acc ctt gac tgg ggc ccc ggt 288
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95

ggg gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
 100 105 110

att caa gat ggc gta aaa gct gcg gag gaa tat gct aaa tct gga aaa 384
 Ile Gln Asp Gly Val Lys Ala Ala Glu Tyr Ala Lys Ser Gly Lys
 115 120 125

gtt cca gat cca agc tgt act gat aat gct gag ttt caa gtt gtg ctt	432
Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
130 135 140	
att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
act gat gtt tgt gac acc gtg atc aag agc aag att gat aac ttg tac	624
Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
195 200 205	
gga tgc cgc cac tca ctt tcg gat ggt ctc atg agg gct act gat gtt	672
Gly Cys Arg His Ser Leu Ser Asp Gly Leu Met Arg Ala Thr Asp Val	
210 215 220	
cgt cgc ccc tgc aag gta gcg ctt gta ggc ggt tac gga gat gtc ttt	720
Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
aag ggt tgg gtt gct gcc ttg aag caa gct ggt gca cgt gtc atc gtg	768
Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
245 250 255	
act gag atc ccg caa atc tgt gcc gtc caa gct acc atg gaa ggt agt	816
Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
tcg gtc ctt acc ctt gag gat gtc gtt tca gat gtt gat cgc ttc gtt	864
Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
275 280 285	
acg aca acc ggt aac aag gac ctc atc atg gtt gac cac atg agg cga	912
Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
290 295 300	
atg aag aac cag gcc ata gtt tgc aac att cga cgt ttc gac aat gaa	960
Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
305 310 315 320	
atc gac atg cgc agt ctc gag acc ttc cct gga gtg aag cgg atc aca	1008
Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
325 330 335	
atc aag gcc cag act gac aga tgg gtc ttt cgc gac acc aac aga ggt	1056
Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
atc att gtc cca gcc gag ggg cgt ctc atg acg atg gga tgc gcc act	1104

Ile Ile Val Pro Ala Glu Gly Arg Leu Met Thr Met Gly Cys Ala Thr
 355 360 365
 gga cac ccc agc ttc cgg acg tcc tgc tct ttc act aac caa gtc agt 1152
 Gly His Pro Ser Phe Arg Thr Ser Cys Ser Phe Thr Asn Gln Val Ser
 370 375 380
 tct cag ctc gag ttg tgg cgg gag aag agc acc ggc aag tat gag aag 1200
 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
 385 390 395 400
 aaa gtg tac gtc ttc cca aag cac ctt gag aag aag gtt gcc gcc ctt 1248
 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
 405 410 415
 cat ctc gta aag ctc gga gca agg ctc act aag ctt agt cgg tgc acg 1296
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
 420 425 430
 ttg ttg tgc acg gac gac cca gtt gaa ggt cgt aaa gag cct cct cac 1344
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
 435 440 445
 cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392
 Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
 450 455 460
 tag taa 1398
 465

<210> 52
 <211> 464
 <212> PRT
 <213> Arabidopsis thaliana

<400> 52
 Met Pro Arg Arg Arg Thr Cys Cys Arg Arg Glu Phe Gly Pro Thr Gln
 1 5 10 15
 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
 20 25 30
 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
 35 40 45
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

100					105					110					
Ile	Gln	Asp	Gly	Val	Lys	Ala	Ala	Glu	Glu	Tyr	Ala	Lys	Ser	Gly	Lys
	115						120					125			
Val	Pro	Asp	Pro	Ser	Cys	Thr	Asp	Asn	Ala	Glu	Phe	Gln	Val	Val	Leu
	130					135					140				
Ile	Ile	Ile	Arg	Glu	Gly	Leu	Lys	Thr	Asp	Pro	Leu	Lys	Tyr	Thr	Lys
	145					150					155				160
Arg	Pro	Ser	Cys	Leu	Val	Gly	Val	Ser	Glu	Glu	Thr	Thr	Thr	Gly	Val
				165					170					175	
Lys	Arg	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Cys	Thr	Leu	Leu	Leu	His	Ala
			180					185					190		
Thr	Asp	Val	Cys	Asp	Thr	Val	Ile	Lys	Ser	Lys	Ile	Asp	Asn	Leu	Tyr
		195					200					205			
Gly	Cys	Arg	His	Ser	Leu	Ser	Asp	Gly	Leu	Met	Arg	Ala	Thr	Asp	Val
	210					215					220				
Arg	Arg	Pro	Cys	Lys	Val	Ala	Leu	Val	Gly	Gly	Tyr	Gly	Asp	Val	Phe
	225					230					235				240
Lys	Gly	Trp	Val	Ala	Ala	Leu	Lys	Gln	Ala	Gly	Ala	Arg	Val	Ile	Val
				245					250					255	
Thr	Glu	Ile	Pro	Gln	Ile	Cys	Ala	Val	Gln	Ala	Thr	Met	Glu	Gly	Ser
			260					265					270		
Ser	Val	Leu	Thr	Leu	Glu	Asp	Val	Val	Ser	Asp	Val	Asp	Arg	Phe	Val
		275					280					285			
Thr	Thr	Thr	Gly	Asn	Lys	Asp	Leu	Ile	Met	Val	Asp	His	Met	Arg	Arg
		290				295						300			
Met	Lys	Asn	Gln	Ala	Ile	Val	Cys	Asn	Ile	Arg	Arg	Phe	Asp	Asn	Glu
				310							315				320
Ile	Asp	Met	Arg	Ser	Leu	Glu	Thr	Phe	Pro	Gly	Val	Lys	Arg	Ile	Thr
				325					330					335	
Ile	Lys	Ala	Gln	Thr	Asp	Arg	Trp	Val	Phe	Arg	Asp	Thr	Asn	Arg	Gly
			340					345					350		
Ile	Ile	Val	Pro	Ala	Glu	Gly	Arg	Leu	Met	Thr	Met	Gly	Cys	Ala	Thr
		355					360					365			
Gly	His	Pro	Ser	Phe	Arg	Thr	Ser	Cys	Ser	Phe	Thr	Asn	Gln	Val	Ser
		370				375					380				
Ser	Gln	Leu	Glu	Leu	Trp	Arg	Glu	Lys	Ser	Thr	Gly	Lys	Tyr	Glu	Lys
				385		390					395				400
Lys	Val	Tyr	Val	Phe	Pro	Lys	His	Leu	Glu	Lys	Lys	Val	Ala	Ala	Leu

405 410 415
 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
 420 425 430
 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
 435 440 445
 Arg Ala Gly Ser Pro Glu Pro Cys Gln Leu Gln Leu Thr Val Phe Arg
 450 455 460

<210> 53
 <211> 771
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(537)

<400> 53
 atg ccg cgt aac gtt gct ggt atg tgc gtt gcg tta gaa cga gtc ttc 48
 Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
 1 5 10 15
 gac gtc gat gaa att gtc agg tta agg aag agg ttt ttc aag ttg gac 96
 Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
 20 25 30
 aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct 144
 Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
 35 40 45
 caa gtt agt tgc aac cct ctt cgg atg cgt gag atg cgt aat ttc gat 192
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
 50 55 60
 aat gat tgc gta ggg agt gtg gat ttt atc gag ttc atc aat gga cgt 240
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
 65 70 75 80
 tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca 288
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
 85 90 95
 ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag 336
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
 100 105 110
 tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat 384
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
 115 120 125
 cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac 432
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp

130 135 140
 ggg gat ggt cga ggt gcg aaa aac agc ttt gag gaa ttt tac ggt cgt 480
 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
 145 150 155 160
 ttg cca gct acc gta cgt cgg cgt ccg tac cgt acg ttg gta agc ggt 528
 Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
 165 170 175
 gat gtg taa agttcagtgc accgtgaccg tgagcctgga agcctgaacg 577
 Asp Val
 ctgacaagcc cttaagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637
 ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697
 cttgagcctg agcctgagcc tgatcgatca aaaaaaaagg agcctttttt ttttagctaa 757
 aaaaaaaaag ctaa 771

<210> 54
 <211> 178
 <212> PRT
 <213> Arabidopsis thaliana

<400> 54
 Met Pro Arg Asn Val Ala Gly Met Cys Val Ala Leu Glu Arg Val Phe
 1 5 10 15
 Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp
 20 25 30
 Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro
 35 40 45
 Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
 50 55 60
 Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
 65 70 75 80
 Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
 85 90 95
 Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
 100 105 110
 Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
 115 120 125
 Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
 130 135 140
 Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
 145 150 155 160

Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
 165 170 175

Asp Val

<210> 55

<211> 1617

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (10) .. (1557)

<400> 55

cgctacgggt atg cgt acg tca aga aca gga ttt cgg atg cca ttg ggg ccc 51
 Met Arg Thr Ser Arg Thr Gly Phe Arg Met Pro Leu Gly Pro
 1 5 10

tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt 99
 Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val
 15 20 25 30

ggc ttc ggc gac gca atc ttc tac gag tgc ttc gcc ggg gat ttt gat 147
 Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp
 35 40 45

gca cgc tgg att tta tcc ggc tca aag tgt ctc tgc gat tgc gcc aag 195
 Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys
 50 55 60

aat gct ggg ttt gat gat tat gga ctt ctt gtg ggt gaa caa gcc agg 243
 Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg
 65 70 75

aag cct cct ata gtc aag gaa ctt gcc gag tct ctc agt cta aag gac 291
 Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp
 80 85 90

gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339
 Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp
 95 100 105 110

tgt gga ggt ccc tgt att aga tat ctt cga acc cag gag agc gga tgg 387
 Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp
 115 120 125

aaa ttt gac agc tcc acc atg ttt ggt gct gct aag tat ggc gcg agg 435
 Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg
 130 135 140

agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483
 Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu
 145 150 155

tgt gtt gac cat gat cac aac cag cgg gct tcc ctc aca tcg gac aaa	531
Cys Val Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys	
160 165 170	
gta cct cgt ttg tac act gga att ctg tcg ccc gaa aat gaa ttc cag	579
Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
gag gac ttt gag cct cct gtt ata cca tcc aag aga agc cct gat aat	675
Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
210 215 220	
ccg tcg aag cgg act gag gac tcg gac gaa aaa gcc aaa atc cca ggc	723
Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
225 230 235	
cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
240 245 250	
atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
255 260 265 270	
gca aaa gac cag gca cac gaa cct gag cca aaa cac tgg ggt gct gaa	867
Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
aag gat ggt gaa tgc gca ccc cca aag att gaa aac gca aag cgg ggg	915
Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
290 295 300	
gcc gcc cct agt tgt ggt gta tcg gag agg caa acc aag att agt cca	963
Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
305 310 315	
aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
320 325 330	
tgg aaa ccc cgc gag atg cta aac cct gga tcg ttc caa atc gca aaa	1059
Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
335 340 345 350	
ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
355 360 365	
ggc atc cta tta gac act gtg gtg ggg gtt agg ggg gat aca ggt gaa	1155
Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
370 375 380	

gaa tat ggg gaa acc ccg ttg aag acc acg tgt acc gtc gag aag cac 1203
 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
 385 390 395
 agt ttg cag gct caa gag gcg aga acc cgg tca gac gct ggt tca ccc 1251
 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
 400 405 410
 tac acc agg tac gta tct aaa atc ccc ggg aaa gcc gat aat ccc ttc 1299
 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
 415 420 425 430
 tcg agc gag cac aaa tgt aag aat ttc gat ctg att gag gct gag aaa 1347
 Ser Ser Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys
 435 440 445
 cag tgt gcc aat gca gta atc ctg ggt gtt gtg gtt aac tcc ggt tca 1395
 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser
 450 455 460
 att aac tcc gtt gtg tct tgg ggc tac aaa cct ggc acg gtg aac aag 1443
 Ile Asn Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys
 465 470 475
 aac caa gaa cgc aga gca ccc tcc cag cga cgt agt agc gag att gaa 1491
 Asn Gln Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu
 480 485 490
 gga acc caa gac cga cga aaa cag gat gtt ggc cga cgc caa gct gcc 1539
 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
 495 500 505 510
 agc tcg ccc agg cgc tga taattaaatc cgatccgtcc tttaaccccc 1587
 Ser Ser Pro Arg Arg
 515

gttggttcaat accgtttttt ttttatttaa 1617

<210> 56
 <211> 515
 <212> PRT
 <213> Arabidopsis thaliana

<400> 56
 Met Arg Thr Ser Arg Thr Gly Phe Arg Met Pro Leu Gly Pro Trp Ala
 1 5 10 15
 Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val Gly Phe
 20 25 30
 Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp Ala Arg
 35 40 45
 Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys Asn Ala
 50 55 60

Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg Lys Pro
 65 70 75 80
 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg
 85 90 95
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly
 100 105 110
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe
 115 120 125
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr
 130 135 140
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val
 145 150 155 160
 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro
 165 170 175
 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu
 180 185 190
 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp
 195 200 205
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser
 210 215 220
 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser
 225 230 235 240
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu
 245 250 255
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys
 260 265 270
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp
 275 280 285
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala
 290 295 300
 Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro Asn Tyr
 305 310 315 320
 Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile Trp Lys
 325 330 335
 Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys Pro Ala
 340 345 350
 Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln Gly Ile
 355 360 365

Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu Glu Tyr
 370 375 380
 Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His Ser Leu
 385 390 395 400
 Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro Tyr Thr
 405 410 415
 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
 420 425 430
 Glu His Lys Cys Lys Asn Phe Asp Leu Ile Glu Ala Glu Lys Gln Cys
 435 440 445
 Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser Ile Asn
 450 455 460
 Ser Val Val Ser Trp Gly Tyr Lys Pro Gly Thr Val Asn Lys Asn Gln
 465 470 475 480
 Glu Arg Arg Ala Pro Ser Gln Arg Arg Ser Ser Glu Ile Glu Gly Thr
 485 490 495
 Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala Ser Ser
 500 505 510
 Pro Arg Arg
 515

<210> 57
 <211> 1281
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (13)..(1266)

<400> 57
 gctccgctcg ct atg agt tgg cga ccc cgg aag aac gtg ccg atg aaa aca 51
 Met Ser Trp Arg Pro Arg Lys Asn Val Pro Met Lys Thr
 1 5 10

cgg gtg acc agg gac ggt tgg ggg ccc gga aaa acc ggt gtc aca cgc 99
 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg
 15 20 25

ggg tgg tca ccc atg cga tgg gca tgg aag cgg tgg caa gcc gtc ggg 147
 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
 30 35 40 45

gca tgg acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
 50 55 60

acg aca agc acc cgc gcg cgg cgc tac gcg gtc tcg gcc aaa ttc ccg	243
Thr Thr Ser Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro	
65 70 75	
aga tta agt aat aag ggc aaa gat tac atg cgt tgc gtc ctc caa tac	291
Arg Leu Ser Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr	
80 85 90	
acc gtc aaa aat gaa caa aaa gtt gat tgt ggt ggc tca tat atc aag	339
Thr Val Lys Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys	
95 100 105	
tta tta cct tcg aaa ttg cgc acg ggt gat ggt gat ggc gtg tca gaa	387
Leu Leu Pro Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu	
110 115 120 125	
tat tca att atg ttt ggt cca gat tcg aca ggt gca tca cgt act gtt	435
Tyr Ser Ile Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val	
130 135 140	
cgt cga gct cgc aat tat aag ggt aaa cgg cat ttg cgg aaa aaa gaa	483
Arg Arg Ala Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu	
145 150 155	
cag aat aaa gtg gaa aca gat caa tta aca cat cag tat act acg agt	531
Gln Asn Lys Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser	
160 165 170	
tgg tca cca gat tgg acc tac aac gtt cta gta gat aat aag gaa tcg	579
Trp Ser Pro Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser	
175 180 185	
caa gca ggg aac ctt gcc gac gac tgc gag tta ctt cca cag aag cga	627
Gln Ala Gly Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg	
190 195 200 205	
atc ttc cga ccc agc tgc cga aaa caa tcc aaa cca gtc acc tgc gta	675
Ile Phe Arg Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val	
210 215 220	
gac gtc aag cac cac gcc ccc cga cga aat gtg aaa ccc gcc ggg cac	723
Asp Val Lys His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His	
225 230 235	
gat gac att cca gcg cga cgg acg acg ccg gaa gcg gtc cgg aaa ggc	771
Asp Asp Ile Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly	
240 245 250	
cgc acg aac gag cga ccg gac cgg acg tgg gcg acc ggg acg acc cca	819
Arg Thr Asn Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro	
255 260 265	
cgg cca cgg cgt tac aag gga gag acg aag gcc aaa aag cac cca cgg	867
Arg Pro Arg Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg	
270 275 280 285	

ccg gaa tac aaa ggg acc tgg gtc acg ccg tta cag gac aac ccc act 915
 Pro Glu Tyr Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr
 290 295 300

cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala
 305 310 315

ggg aca cgg acc tgg acc gtg aaa tcg ggc tca atc acg aac aac atg 1011
 Gly Thr Arg Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met
 320 325 330

ata gtg aca acg tcc gtg gaa acc gcg acc gac ttc tca gag aaa acc 1059
 Ile Val Thr Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr
 335 340 345

aag gtg gca aac acc acg acc gag ctc aac gac gga cgc gac gcc gga 1107
 Lys Val Ala Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly
 350 355 360 365

acg ggg atc ggt gcc gag cgc cac tgt gct gat gag aga tgg aaa gag 1155
 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu
 370 375 380

aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203
 Thr Thr Val Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg
 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
 Arg Thr Gly Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu
 400 405 410

tac gga ccg gaa taa aatcgccctga tgcct 1281
 Tyr Gly Pro Glu
 415

<210> 58

<211> 417

<212> PRT

<213> Arabidopsis thaliana

<400> 58

Met Ser Trp Arg Pro Arg Lys Asn Val Pro Met Lys Thr Arg Val Thr
 1 5 10 15

Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg Gly Ser Ser
 20 25 30

Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly Ala Ser Thr
 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
 65 70 75 80

Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys
 85 90 95
 Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro
 100 105 110
 Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile
 115 120 125
 Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala
 130 135 140
 Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys
 145 150 155 160
 Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro
 165 170 175
 Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly
 180 185 190
 Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg
 195 200 205
 Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys
 210 215 220
 His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile
 225 230 235 240
 Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn
 245 250 255
 Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg
 260 265 270
 Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr
 275 280 285
 Lys Gly Thr Trp Val Thr Pro Leu Gln Asp Asn Pro Thr Pro Ala Pro
 290 295 300
 Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala Gly Thr Arg
 305 310 315 320
 Thr Trp Thr Val Lys Ser Gly Ser Ile Thr Asn Asn Met Ile Val Thr
 325 330 335
 Thr Ser Val Glu Thr Ala Thr Asp Phe Ser Glu Lys Thr Lys Val Ala
 340 345 350
 Asn Thr Thr Thr Glu Leu Asn Asp Gly Arg Asp Ala Gly Thr Gly Ile
 355 360 365
 Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu Thr Thr Val
 370 375 380

Ala Pro Asp Cys Ala Val Ser Ala Ala Asn Ala Ser Arg Arg Thr Gly
385 390 395 400

Glu Leu Ala Thr Pro Val Thr Met Leu Pro Asp Pro Leu Tyr Gly Pro
405 410 415

Glu

<210> 59

<211> 416

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(411)

<400> 59

aag gaa gct ttt agc ctc ttc gac aaa gat ggc gat ggt tgc atc aca 48
Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr
1 5 10 15

aca aaa gag ctg gga aca gtt atg cgt tca cta gga caa aac cca aca 96
Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr
20 25 30

gag gct gag ctc caa gac atg atc aac gag gtt gat gca gat gga aac 144
Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn
35 40 45

ggc act atc gac ttc ccc gag ttc ctg aac ctg atg gct aag aag atg 192
Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
50 55 60

aaa gac act gac tcc gag gaa gag cta aaa gaa gcc ttc agg gtt ttc 240
Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
65 70 75 80

gac aaa gac cag aac ggt ttc atc tcc gct gct gag cta cgc cat gtg 288
Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
85 90 95

atg acc aat ctt ggt gag aag cta act gat gaa gaa gtg gaa gag atg 336
Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
100 105 110

atc cgt gag gct gat gtt gat gga gat ggt cag att aac tat gaa gag 384
Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
115 120 125

ttt gtc aag att atg atg gct aag tga tttgat 417
Phe Val Lys Ile Met Met Ala Lys
130 135

<210> 60
 <211> 136
 <212> PRT
 <213> Arabidopsis thaliana

<400> 60
 Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr
 1 5 10 15
 Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr
 20 25 30
 Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn
 35 40 45
 Gly Thr Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Lys Lys Met
 50 55 60
 Lys Asp Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe
 65 70 75 80
 Asp Lys Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val
 85 90 95
 Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Glu Glu Met
 100 105 110
 Ile Arg Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu
 115 120 125
 Phe Val Lys Ile Met Met Ala Lys
 130 135

<210> 61
 <211> 6069
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (34)..(173)

<220>
 <221> CDS
 <222> (282)..(492)

<220>
 <221> CDS
 <222> (539)..(1135)

<220>
 <221> CDS
 <222> (1224)..(1320)

<220>
<221> CDS
<222> (1404) .. (1585)

<220>
<221> CDS
<222> (1663) .. (1778)

<220>
<221> CDS
<222> (1891) .. (1993)

<220>
<221> CDS
<222> (2114) .. (2266)

<220>
<221> CDS
<222> (2376) .. (2522)

<220>
<221> CDS
<222> (2608) .. (2808)

<220>
<221> CDS
<222> (3071) .. (3235)

<220>
<221> CDS
<222> (3315) .. (3419)

<220>
<221> CDS
<222> (3519) .. (3656)

<220>
<221> CDS
<222> (3742) .. (3936)

<220>
<221> CDS
<222> (4061) .. (4187)

<220>
<221> CDS
<222> (4268) .. (4470)

<220>
<221> CDS
<222> (4556) .. (4738)

<220>
<221> CDS
<222> (4809) .. (4904)

<220>

<221> CDS

<222> (4991)..(5188)

<220>

<221> CDS

<222> (5509)..(5780)

<220>

<221> CDS

<222> (5879)..(6059)

<400> 61

cagatctact acaatctctc tttttcttcg ggt atg gag ggc caa cga ggc agt 54

Met Glu Gly Gln Arg Gly Ser

1

5

aat tct tcg ttg agc tct ggc aat ggc acc gaa gtc gcc acc gac gtt 102

Asn Ser Ser Leu Ser Ser Gly Asn Gly Thr Glu Val Ala Thr Asp Val

10

15

20

tct tct tgc ttc tat gtt ccc aat ccc tct gga acc gat ttc gat gcc 150

Ser Ser Cys Phe Tyr Val Pro Asn Pro Ser Gly Thr Asp Phe Asp Ala

25

30

35

gag tcg tct tct ctt cct cct ct gtaagtcttc ttgaatttt taaaaacatt 203

Glu Ser Ser Ser Leu Pro Pro Le

40

45

cactctcttg ctgctgtctc tgttgatcct tcttctttga aaatttgaaa acattcttag 263

tctctcgctc tgtcacag c tcc cca gct cct caa gtg gca ttg tca att cct 315

u Ser Pro Ala Pro Gln Val Ala Leu Ser Ile Pro

50

55

gcg gag ctt gcc gcc gcc att ccc ctc atc gat cgc ttc cag gtt gaa 363

Ala Glu Leu Ala Ala Ala Ile Pro Leu Ile Asp Arg Phe Gln Val Glu

60

65

70

gct ttt ctg cgg cta atg cag aaa caa atc cag tct gct ggg aag cgt 411

Ala Phe Leu Arg Leu Met Gln Lys Gln Ile Gln Ser Ala Gly Lys Arg

75

80

85

90

ggc ttc ttc tat tcc aaa aag tcc tct ggc tcc aat gtc cgc gag cgc 459

Gly Phe Phe Tyr Ser Lys Lys Ser Ser Gly Ser Asn Val Arg Glu Arg

95

100

105

ttc aca ttt gag gat atg ctt tgc ttt caa aag gtttttcttt ccccccttt 512

Phe Thr Phe Glu Asp Met Leu Cys Phe Gln Lys

110

115

cttccccatt gacaatccat tgactg aat atg tct ctc tcc cct tcc ttc ctt 565

Asn Met Ser Leu Ser Pro Ser Phe Leu

120

125

cag gat cca atc ccc aca tct ctc ctc aag att aac agc gat ctc gtc 613

Gln Asp Pro Ile Pro Thr Ser Leu Leu Lys Ile Asn Ser Asp Leu Val

130

135

140

agc cgt gct acc aag ttg ttt cat ctc atc tta aaa tat atg ggt gtt 661
 Ser Arg Ala Thr Lys Leu Phe His Leu Ile Leu Lys Tyr Met Gly Val
 145 150 155

gat tca tct gat cga tct acg cct ccc agt tta gat gaa cgc att gac 709
 Asp Ser Ser Asp Arg Ser Thr Pro Pro Ser Leu Asp Glu Arg Ile Asp
 160 165 170

ctc gtt gga aag ctc ttc aaa aaa act ttg aag cgt gtt gaa ctc agg 757
 Leu Val Gly Lys Leu Phe Lys Lys Thr Leu Lys Arg Val Glu Leu Arg
 175 180 185 190

gac gaa ctt ttt gcc caa atc tcc aaa cag act aga cat aat cct gac 805
 Asp Glu Leu Phe Ala Gln Ile Ser Lys Gln Thr Arg His Asn Pro Asp
 195 200 205

agg caa tac ttg atc aaa gct tgg gaa ttg atg tac tta tgt gcc tcc 853
 Arg Gln Tyr Leu Ile Lys Ala Trp Glu Leu Met Tyr Leu Cys Ala Ser
 210 215 220

tct atg cct cct agc aaa gat atc ggt gga tat cta tct gag tat att 901
 Ser Met Pro Pro Ser Lys Asp Ile Gly Gly Tyr Leu Ser Glu Tyr Ile
 225 230 235

cat aat gtc gca cac gat gca act att gaa ccg gat gct cag gtt ctt 949
 His Asn Val Ala His Asp Ala Thr Ile Glu Pro Asp Ala Gln Val Leu
 240 245 250

gct gtt aac act ttg aaa gct tta aag cgc tct atc aaa gct ggt cct 997
 Ala Val Asn Thr Leu Lys Ala Leu Lys Arg Ser Ile Lys Ala Gly Pro
 255 260 265 270

agg cac acc aca cct ggt cgt gaa gaa att gaa gcc ctt ttg acc ggt 1045
 Arg His Thr Thr Pro Gly Arg Glu Glu Ile Glu Ala Leu Leu Thr Gly
 275 280 285

aga aag ctc aca acc att gtc ttc ttt ctc gat gaa act ttt gaa gaa 1093
 Arg Lys Leu Thr Thr Ile Val Phe Phe Leu Asp Glu Thr Phe Glu Glu
 290 295 300

att tca tat gac atg gct acc aca gtg tct gat gct gtt gag 1135
 Ile Ser Tyr Asp Met Ala Thr Thr Val Ser Asp Ala Val Glu
 305 310 315

gtatcttctt gctttctttt ttcataattt accgctgac atattcttgt ccctttttct 1195

ctcaactgcat tgacatctgt ttcaggag cta gct gga aca att aaa cta tca 1247
 Leu Ala Gly Thr Ile Lys Leu Ser
 320

gct ttc tct agc ttt agt ttg ttt gaa tgt cgt aaa gtt gtt tca agt 1295
 Ala Phe Ser Ser Phe Ser Leu Phe Glu Cys Arg Lys Val Val Ser Ser
 325 330 335 340

tct aaa tca tct gat ccc gga aat g gtatgctttc atatgactgg 1340
 Ser Lys Ser Ser Asp Pro Gly Asn G

345

cttcgtcata tattgtgaag taatacaaca ttatcgatca tttttctatc tgtgcacttg 1400

cag ag gaa tat ata gga ttg gat gat aac aag tat att gga gat ctc 1447
 lu Glu Tyr Ile Gly Leu Asp Asp Asn Lys Tyr Ile Gly Asp Leu
 350 355 360

ctc gca gaa ttt aaa gct att aaa gac cga aat aaa gga gag ata cta 1495
 Leu Ala Glu Phe Lys Ala Ile Lys Asp Arg Asn Lys Gly Glu Ile Leu
 365 370 375

cac tgc aaa ctg gta ttt aaa aaa aaa tta ttc cga gag tct gat gaa 1543
 His Cys Lys Leu Val Phe Lys Lys Lys Leu Phe Arg Glu Ser Asp Glu
 380 385 390 395

gct gta acg gat ctg atg ttt gtg caa ctt tcg tat gtt caa 1585
 Ala Val Thr Asp Leu Met Phe Val Gln Leu Ser Tyr Val Gln
 400 405

gtgagcattt tcttcattgg tgacatttat ttccacacaa aaggcttgcc tttcgttgct 1645

gacacacata tatgcag ctg caa cat gac tat ttg cta gga aac tat cct 1695
 Leu Gln His Asp Tyr Leu Leu Gly Asn Tyr Pro
 410 415 420

gtt ggg agg gac gat gct gca cag ctt tgt gcc ttg caa att ctt gtt 1743
 Val Gly Arg Asp Ala Ala Gln Leu Cys Ala Leu Gln Ile Leu Val
 425 430 435

ggg att ggg ttt gtc aat agt cca gag tca tgc at gttagttttc 1788
 Gly Ile Gly Phe Val Asn Ser Pro Glu Ser Cys Il
 440 445

ttaagctccg ccattgactt tatttttagtt gtccgatact ttatttttcc aattttcctc 1848

ccttaacaat atcatttcct ttctcaatgt atcacatata ag t gat tgg aca tca 1903
 e Asp Trp Thr Ser
 450

ctt ctt gag cgg ttt ttg cca aga caa ata gca ata acc cga gca aag 1951
 Leu Leu Glu Arg Phe Leu Pro Arg Gln Ile Ala Ile Thr Arg Ala Lys
 455 460 465

cgt gaa tgg gaa ttg gat atc ctt gct cgc tac cgt tca atg 1993
 Arg Glu Trp Glu Leu Asp Ile Leu Ala Arg Tyr Arg Ser Met
 470 475 480

gtaggaatag ttctatgcat gtggattgtc ttcccccttc tagatacctt tggcaaataa 2053

aaacccattg aagtgatggc atggtaaaat gatatttcgt atgtgtatgt gggcatgtag 2113

gag aac gtg acc aaa gat gat gca aga caa caa ttt cta cgg ata ctg 2161
 Glu Asn Val Thr Lys Asp Asp Ala Arg Gln Gln Phe Leu Arg Ile Leu
 485 490 495

aag gca ctg cca tac ggg aat tca gtt ttt ttt agc gta cgc aag ata 2209

Lys Ala Leu Pro Tyr Gly Asn Ser Val Phe Phe Ser Val Arg Lys Ile
 500 505 510
 gat gat ccg atc ggt ctt tta cct ggg cga atc att ttg ggt atc aac 2257
 Asp Asp Pro Ile Gly Leu Leu Pro Gly Arg Ile Ile Leu Gly Ile Asn
 515 520 525 530
 aaa cgt ggg gttgtctcaa tataaatggt atacattatg actttaaaaa 2306
 Lys Arg Gly
 aactgttatt gttgtttgga attcaaatct atgttggttg atttgaattt gttgtttgct 2366
 ttctttagtag gtt cac ttt ttt cga ccg gtt cct aaa gaa tat ctg cac tct 2417
 Val His Phe Phe Arg Pro Val Pro Lys Glu Tyr Leu His Ser
 535 540 545
 gct gaa cta cgt gac atc atg caa ttt ggc agc agt aac act gct gtc 2465
 Ala Glu Leu Arg Asp Ile Met Gln Phe Gly Ser Ser Asn Thr Ala Val
 550 555 560
 ttt ttc aaa atg aga gtc gct ggt gtt ctt cac ata ttt cag ttc gag 2513
 Phe Phe Lys Met Arg Val Ala Gly Val Leu His Ile Phe Gln Phe Glu
 565 570 575
 aca aaa cag gtttaaacad cactatttgt ggatcattat attatgaagc 2562
 Thr Lys Gln
 580
 aattcccttat gagatattca atttgggtaa cttgtatggt tgtag gga gaa gaa att 2619
 Gly Glu Glu Ile
 585
 tgt gtt gct ttg caa aca cat ata aat gat gtc atg ttg cgt cgt tac 2667
 Cys Val Ala Leu Gln Thr His Ile Asn Asp Val Met Leu Arg Arg Tyr
 590 595 600
 tcc aaa gct cga tct gct gcc aat tgc ttg gtt aat gga gat att tct 2715
 Ser Lys Ala Arg Ser Ala Ala Asn Cys Leu Val Asn Gly Asp Ile Ser
 605 610 615
 tgt tgt tct aag ccg caa aat ttt gaa gtg tat gaa aaa cgt ttg caa 2763
 Cys Cys Ser Lys Pro Gln Asn Phe Glu Val Tyr Glu Lys Arg Leu Gln
 620 625 630
 gat ttg tct aag gct tat gaa gag tcc caa aag aag att gag aag 2808
 Asp Leu Ser Lys Ala Tyr Glu Glu Ser Gln Lys Lys Ile Glu Lys
 635 640 645
 gtacacattc taacaaattt cttatttatt cttcaatgta aaattgaata taatagaggg 2868
 aggctgatct ttgtttaaat acatgaaata acttattgta gttggatttt ttcattggtt 2928
 ttatgcttgg tagtcttgag atatttcagt atatatcacc ctccatctt atgttattgt 2988
 atgtagaatg ttataccatg acctcttttg ttttagagtg gcatgctgat gaactattcg 3048
 tatgttttat gttgttgtat ag ttg atg gat gaa caa caa gag aaa aat cag 3100

Leu Met Asp Glu Gln Gln Glu Lys Asn Gln
 650 655

caa gaa gtt act ctg cgt gaa gag tta gaa gct ata cac aat ggt ttg 3148
 Gln Glu Val Thr Leu Arg Glu Glu Leu Glu Ala Ile His Asn Gly Leu
 660 665 670 675

gag ctt gaa agg aga aaa ttg ttg gag gtt act tta gac cga gat aaa 3196
 Glu Leu Glu Arg Arg Lys Leu Leu Glu Val Thr Leu Asp Arg Asp Lys
 680 685 690

ctt agg tca ttg tgt gac gag aag gga acc cct att caa gttagttata 3245
 Leu Arg Ser Leu Cys Asp Glu Lys Gly Thr Pro Ile Gln
 695 700

acctaaacttt tgccttttctt ttgatgcttg gttgaagtta tttaatgatt tattctatat 3305

atgctatag tcc ttg atg tct gaa ctg cga gga atg gaa gca agg ttg gca 3356
 Ser Leu Met Ser Glu Leu Arg Gly Met Glu Ala Arg Leu Ala
 705 710 715

aag tcg ggc aac acc aaa tca agt aaa gag acc aaa tca gaa tta gcc 3404
 Lys Ser Gly Asn Thr Lys Ser Ser Lys Glu Thr Lys Ser Glu Leu Ala
 720 725 730

gaa atg aat aat cag gtgaatatta tgtgttttaa tctaattcat tgtaatcatt 3459
 Glu Met Asn Asn Gln
 735

gagttgttgt tttttgttcc caattctgct ttcttttgac aatgaatttt aagtcacag 3518

ata tta tac aag atc caa aag gag tta gaa gtt cga aat aag gaa ttg 3566
 Ile Leu Tyr Lys Ile Gln Lys Glu Leu Glu Val Arg Asn Lys Glu Leu
 740 745 750 755

cat gtc gca gtt gat aat tca aag agg ttg ttg agt gaa aac aag ata 3614
 His Val Ala Val Asp Asn Ser Lys Arg Leu Leu Ser Glu Asn Lys Ile
 760 765 770

ttg gag caa aat ctc aat att gaa aag aag aaa aaa gag gag 3656
 Leu Glu Gln Asn Leu Asn Ile Glu Lys Lys Lys Lys Glu Glu
 775 780 785

gtgaattcta tgtattagat ttattgaaga tttcaaattg agaagtatca aatacttgcg 3716

tattgttgac atctcattat ttcag gtt gaa att cat caa aag aga tat gaa 3768
 Val Glu Ile His Gln Lys Arg Tyr Glu
 790

caa gaa aaa aag gtg tta aag ctt cga gtt tct gaa ctt gaa aat aag 3816
 Gln Glu Lys Lys Val Leu Lys Leu Arg Val Ser Glu Leu Glu Asn Lys
 795 800 805 810

ctt gaa gta ctt gct caa gac ttg gat agt gct gag tct acg att gaa 3864
 Leu Glu Val Leu Ala Gln Asp Leu Asp Ser Ala Glu Ser Thr Ile Glu
 815 820 825

agt aag aat tct gac atg ctg ctg ttg caa aat aac ttg aaa gaa ctt 3912
 Ser Lys Asn Ser Asp Met Leu Leu Leu Gln Asn Asn Leu Lys Glu Leu
 830 835 840

gag gag tta aga gaa atg aaa gag gtaatggtac tcttttgtct tcttcattat 3966
 Glu Glu Leu Arg Glu Met Lys Glu
 845 850

ttaattttgt ttctgtttga atgatgataa tgtattttcg cgattccaaa ttgaagtaga 4026
 gggatgtgtt tacattccaa tttcattttc ttag gac att gac aga aaa aat gag 4081
 Asp Ile Asp Arg Lys Asn Glu
 855

caa aca gct gcc att ttg aaa atg caa gga gcc caa ctt gct gag cta 4129
 Gln Thr Ala Ala Ile Leu Lys Met Gln Gly Ala Gln Leu Ala Glu Leu
 860 865 870

gaa ata ctt tat aag gaa gaa caa gtt tta agg aaa aga tac tat aat 4177
 Glu Ile Leu Tyr Lys Glu Glu Gln Val Leu Arg Lys Arg Tyr Tyr Asn
 875 880 885

acc ata gaa g gtaacataat gctcaagtat gtacaatgat gttcattgct 4227
 Thr Ile Glu A
 890

tttaaaaaag aattttacta acatttttat ttgattgtag at atg aaa ggg aag 4281
 sp Met Lys Gly Lys
 895

att aga gtt tat tgt cga ata aga cct cta aat gaa aaa gag agt tca 4329
 Ile Arg Val Tyr Cys Arg Ile Arg Pro Leu Asn Glu Lys Glu Ser Ser
 900 905 910

gag agg gaa aaa caa atg ctg aca act gtg gat gag ttt act gtt gaa 4377
 Glu Arg Glu Lys Gln Met Leu Thr Thr Val Asp Glu Phe Thr Val Glu
 915 920 925

cat gca tgg aaa gac gac aaa aga aag caa cac ata tat gat cgc gta 4425
 His Ala Trp Lys Asp Asp Lys Arg Lys Gln His Ile Tyr Asp Arg Val
 930 935 940 945

ttt gac atg cgt gct agt caa gat gat atc ttt gaa gac aca aag 4470
 Phe Asp Met Arg Ala Ser Gln Asp Asp Ile Phe Glu Asp Thr Lys
 950 955 960

gtattattga tatgtaactg tgttcattta cctttcatcc tttgttattt tcttgtggtt 4530

actaacatcg ttttcctttt aacag tat ttg gta cag tcc gct gta gat ggg 4582
 Tyr Leu Val Gln Ser Ala Val Asp Gly
 965

tat aac gtt tgc atc ttt gca tat ggt caa act ggt tct gga aaa act 4630
 Tyr Asn Val Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser Gly Lys Thr
 970 975 980 985

ttc act ata tat ggg cat gag agc aat cct gga ctc aca cct cga gct 4678

Phe Thr Ile Tyr Gly His Glu Ser Asn Pro Gly Leu Thr Pro Arg Ala
 990 995 1000
 aca aag gaa ctg ttc aac ata tta aag cga gat agc aag aga ttt tca 4726
 Thr Lys Glu Leu Phe Asn Ile Leu Lys Arg Asp Ser Lys Arg Phe Ser
 1005 1010 1015
 ttt tct cta aag gtaatttgtt atcctaataag atgatgtgat aaaagattat 4778
 Phe Ser Leu Lys
 1020
 gacatcaact gactacaaaa agttatgcag gca tat atg gtg gaa ctt tat caa 4832
 Ala Tyr Met Val Glu Leu Tyr Gln
 1025
 gac aca ctt gta gac ctt ttg tta cca aaa agt gca aga cgc ttg aaa 4880
 Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser Ala Arg Arg Leu Lys
 1030 1035 1040 1045
 cta gag att aaa aaa gat tca aag gtattgtgag atatattctat tttaactagg 4934
 Leu Glu Ile Lys Lys Asp Ser Lys
 1050
 ttataactag attgtagaca cgtaagtttg atcttatgca taaaatattt tctcag gga 4993
 Gly
 atg gtc ttt gta gag aat gtg aca act att cct ata tca act ttg gag 5041
 Met Val Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu
 1055 1060 1065 1070
 gaa ctg cga atg att ctt gaa cgg gga tcg gaa cga cga cat gtt tct 5089
 Glu Leu Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser
 1075 1080 1085
 gga aca aat atg aat gaa gaa agc tca aga tct cac ctc ata tta tca 5137
 Gly Thr Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser
 1090 1095 1100
 gtt gtt att gaa agt att gat ctt caa acc cag tct gct gcg agg ggc 5185
 Val Val Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly
 1105 1110 1115
 aag gtgacaaaat tcactatggt tttcttttatt gactcattat cattttttcac 5238
 Lys
 aggatttagt agcatttagg gattttaagg aaataggagt ttcttttagat tttcatgctt 5298
 agtctaccga agaaaaatat agtaacatta atcttggtta agagagatat tatttttacag 5358
 ctcaaatctt tggctctgga caaaatgtta aacctttatg tacacaatcc atattattag 5418
 tcaatgatat gccctccatt gttaaaccga tatcacctga tcatggtggt atcttctaca 5478
 atattctgaa tttttgtttg ttatttgcag ctg agt ttt gtg gat ctt gct ggt 5532
 Leu Ser Phe Val Asp Leu Ala Gly
 1120 1125

tct gag aga gtt aaa aag tgc ggc tca gct ggt tgc caa ctc aaa gaa 5580
 Ser Glu Arg Val Lys Lys Ser Gly Ser Ala Gly Cys Gln Leu Lys Glu
 1130 1135 1140

gct caa agt atc aac aaa tca ctt tct gca tta ggt gat gtt att ggt 5628
 Ala Gln Ser Ile Asn Lys Ser Leu Ser Ala Leu Gly Asp Val Ile Gly
 1145 1150 1155

gct tta tct tct ggc aac cag cat att cct tat agg aat cac aag cta 5676
 Ala Leu Ser Ser Gly Asn Gln His Ile Pro Tyr Arg Asn His Lys Leu
 1160 1165 1170 1175

acg atg ttg atg agc gat tca ttg ggc ggc aat gcc aag acg tta atg 5724
 Thr Met Leu Met Ser Asp Ser Leu Gly Gly Asn Ala Lys Thr Leu Met
 1180 1185 1190

ttt gtt aat gtg tct cca gcc gaa tca aat ttg gac gag acg tac aat 5772
 Phe Val Asn Val Ser Pro Ala Glu Ser Asn Leu Asp Glu Thr Tyr Asn
 1195 1200 1205

tct ctt ct gtaagtcag agttcccata tatatataac ataaatcaaa tatgcttagt 5830
 Ser Leu Le

gtaaaaatgg ataatccata ttgttttttt ttcttccttt gattccag a tat gca 5885
 u Tyr Ala
 1210

tcg aga gtg aga acg atc gtg aat gat ccc agc aaa cat ata tca tcc 5933
 Ser Arg Val Arg Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser
 1215 1220 1225

aaa gag atg gtg cga ttg aag aag ttg gta gca tac tgg aaa gag caa 5981
 Lys Glu Met Val Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln
 1230 1235 1240

gcc ggt aaa aaa ggt gag gaa gaa gac ttg gtg gat att gag gaa gat 6029
 Ala Gly Lys Lys Gly Glu Glu Glu Asp Leu Val Asp Ile Glu Glu Asp
 1245 1250 1255 1260

cgt aca cga aaa gat gag gca gat agt tga agaaagctga c 6070
 Arg Thr Arg Lys Asp Glu Ala Asp Ser
 1265 1270

<210> 62

<211> 1269

<212> PRT

<213> Arabidopsis thaliana

<400> 62

Met Glu Gly Gln Arg Gly Ser Asn Ser Ser Leu Ser Ser Gly Asn Gly
 1 5 10 15

Thr Glu Val Ala Thr Asp Val Ser Ser Cys Phe Tyr Val Pro Asn Pro
 20 25 30

Ser Gly Thr Asp Phe Asp Ala Glu Ser Ser Ser Leu Pro Pro Leu Ser

35					40					45				
Pro	Ala	Pro	Gln	Val	Ala	Leu	Ser	Ile	Pro	Ala	Glu	Leu	Ala	Ala
50					55					60				
Ile	Pro	Leu	Ile	Asp	Arg	Phe	Gln	Val	Glu	Ala	Phe	Leu	Arg	Leu
65					70					75				80
Gln	Lys	Gln	Ile	Gln	Ser	Ala	Gly	Lys	Arg	Gly	Phe	Phe	Tyr	Ser
				85					90					95
Lys	Ser	Ser	Gly	Ser	Asn	Val	Arg	Glu	Arg	Phe	Thr	Phe	Glu	Asp
			100					105					110	Met
Leu	Cys	Phe	Gln	Lys	Asn	Met	Ser	Leu	Ser	Pro	Ser	Phe	Leu	Gln
		115					120					125		Asp
Pro	Ile	Pro	Thr	Ser	Leu	Leu	Lys	Ile	Asn	Ser	Asp	Leu	Val	Ser
	130						135					140		Arg
Ala	Thr	Lys	Leu	Phe	His	Leu	Ile	Leu	Lys	Tyr	Met	Gly	Val	Asp
145												155		160
Ser	Asp	Arg	Ser	Thr	Pro	Pro	Ser	Leu	Asp	Glu	Arg	Ile	Asp	Leu
				165										175
Gly	Lys	Leu	Phe	Lys	Lys	Thr	Leu	Lys	Arg	Val	Glu	Leu	Arg	Asp
			180						185					190
Leu	Phe	Ala	Gln	Ile	Ser	Lys	Gln	Thr	Arg	His	Asn	Pro	Asp	Arg
		195					200					205		Gln
Tyr	Leu	Ile	Lys	Ala	Trp	Glu	Leu	Met	Tyr	Leu	Cys	Ala	Ser	Ser
	210						215					220		Met
Pro	Pro	Ser	Lys	Asp	Ile	Gly	Gly	Tyr	Leu	Ser	Glu	Tyr	Ile	His
				230								235		240
Val	Ala	His	Asp	Ala	Thr	Ile	Glu	Pro	Asp	Ala	Gln	Val	Leu	Ala
				245					250					255
Asn	Thr	Leu	Lys	Ala	Leu	Lys	Arg	Ser	Ile	Lys	Ala	Gly	Pro	Arg
			260					265					270	His
Thr	Thr	Pro	Gly	Arg	Glu	Glu	Ile	Glu	Ala	Leu	Leu	Thr	Gly	Arg
		275					280						285	Lys
Leu	Thr	Thr	Ile	Val	Phe	Phe	Leu	Asp	Glu	Thr	Phe	Glu	Glu	Ile
							295					300		Ser
Tyr	Asp	Met	Ala	Thr	Thr	Val	Ser	Asp	Ala	Val	Glu	Leu	Ala	Gly
				310								315		320
Ile	Lys	Leu	Ser	Ala	Phe	Ser	Ser	Phe	Ser	Leu	Phe	Glu	Cys	Arg
				325					330					335
Val	Val	Ser	Ser	Ser	Lys	Ser	Ser	Asp	Pro	Gly	Asn	Glu	Glu	Tyr
														Ile

132

				645					650					655			
Lys	Asn	Gln	Gln	Glu	Val	Thr	Leu	Arg	Glu	Glu	Leu	Glu	Ala	Ile	His		
			660					665					670				
Asn	Gly	Leu	Glu	Leu	Glu	Arg	Arg	Lys	Leu	Leu	Glu	Val	Thr	Leu	Asp		
		675					680					685					
Arg	Asp	Lys	Leu	Arg	Ser	Leu	Cys	Asp	Glu	Lys	Gly	Thr	Pro	Ile	Gln		
	690					695					700						
Ser	Leu	Met	Ser	Glu	Leu	Arg	Gly	Met	Glu	Ala	Arg	Leu	Ala	Lys	Ser		
	705				710					715					720		
Gly	Asn	Thr	Lys	Ser	Ser	Lys	Glu	Thr	Lys	Ser	Glu	Leu	Ala	Glu	Met		
				725					730					735			
Asn	Asn	Gln	Ile	Leu	Tyr	Lys	Ile	Gln	Lys	Glu	Leu	Glu	Val	Arg	Asn		
			740					745						750			
Lys	Glu	Leu	His	Val	Ala	Val	Asp	Asn	Ser	Lys	Arg	Leu	Leu	Ser	Glu		
	755						760					765					
Asn	Lys	Ile	Leu	Glu	Gln	Asn	Leu	Asn	Ile	Glu	Lys	Lys	Lys	Lys	Glu		
	770					775					780						
Glu	Val	Glu	Ile	His	Gln	Lys	Arg	Tyr	Glu	Gln	Glu	Lys	Lys	Val	Leu		
	785				790					795					800		
Lys	Leu	Arg	Val	Ser	Glu	Leu	Glu	Asn	Lys	Leu	Glu	Val	Leu	Ala	Gln		
				805					810					815			
Asp	Leu	Asp	Ser	Ala	Glu	Ser	Thr	Ile	Glu	Ser	Lys	Asn	Ser	Asp	Met		
			820					825					830				
Leu	Leu	Leu	Gln	Asn	Asn	Leu	Lys	Glu	Leu	Glu	Glu	Leu	Arg	Glu	Met		
		835					840					845					
Lys	Glu	Asp	Ile	Asp	Arg	Lys	Asn	Glu	Gln	Thr	Ala	Ala	Ile	Leu	Lys		
	850					855					860						
Met	Gln	Gly	Ala	Gln	Leu	Ala	Glu	Leu	Glu	Ile	Leu	Tyr	Lys	Glu	Glu		
	865				870					875					880		
Gln	Val	Leu	Arg	Lys	Arg	Tyr	Tyr	Asn	Thr	Ile	Glu	Asp	Met	Lys	Gly		
				885					890					895			
Lys	Ile	Arg	Val	Tyr	Cys	Arg	Ile	Arg	Pro	Leu	Asn	Glu	Lys	Glu	Ser		
			900					905					910				
Ser	Glu	Arg	Glu	Lys	Gln	Met	Leu	Thr	Thr	Val	Asp	Glu	Phe	Thr	Val		
		915					920					925					
Glu	His	Ala	Trp	Lys	Asp	Asp	Lys	Arg	Lys	Gln	His	Ile	Tyr	Asp	Arg		
	930					935					940						
Val	Phe	Asp	Met	Arg	Ala	Ser	Gln	Asp	Asp	Ile	Phe	Glu	Asp	Thr	Lys		

945 950 955 960
 Tyr Leu Val Gln Ser Ala Val Asp Gly Tyr Asn Val Cys Ile Phe Ala
 965 970 975
 Tyr Gly Gln Thr Gly Ser Gly Lys Thr Phe Thr Ile Tyr Gly His Glu
 980 985 990
 Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile
 995 1000 1005
 Leu Lys Arg Asp Ser Lys Arg Phe Ser Phe Ser Leu Lys Ala Tyr Met
 1010 1015 1020
 Val Glu Leu Tyr Gln Asp Thr Leu Val Asp Leu Leu Leu Pro Lys Ser
 1025 1030 1035 1040
 Ala Arg Arg Leu Lys Leu Glu Ile Lys Lys Asp Ser Lys Gly Met Val
 1045 1050 1055
 Phe Val Glu Asn Val Thr Thr Ile Pro Ile Ser Thr Leu Glu Glu Leu
 1060 1065 1070
 Arg Met Ile Leu Glu Arg Gly Ser Glu Arg Arg His Val Ser Gly Thr
 1075 1080 1085
 Asn Met Asn Glu Glu Ser Ser Arg Ser His Leu Ile Leu Ser Val Val
 1090 1095 1100
 Ile Glu Ser Ile Asp Leu Gln Thr Gln Ser Ala Ala Arg Gly Lys Leu
 1105 1110 1115 1120
 Ser Phe Val Asp Leu Ala Gly Ser Glu Arg Val Lys Lys Ser Gly Ser
 1125 1130 1135
 Ala Gly Cys Gln Leu Lys Glu Ala Gln Ser Ile Asn Lys Ser Leu Ser
 1140 1145 1150
 Ala Leu Gly Asp Val Ile Gly Ala Leu Ser Ser Gly Asn Gln His Ile
 1155 1160 1165
 Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly
 1170 1175 1180
 Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser
 1185 1190 1195 1200
 Asn Leu Asp Glu Thr Tyr Asn Ser Leu Leu Tyr Ala Ser Arg Val Arg
 1205 1210 1215
 Thr Ile Val Asn Asp Pro Ser Lys His Ile Ser Ser Lys Glu Met Val
 1220 1225 1230
 Arg Leu Lys Lys Leu Val Ala Tyr Trp Lys Glu Gln Ala Gly Lys Lys
 1235 1240 1245
 Gly Glu Glu Glu Asp Leu Val Asp Ile Glu Glu Asp Arg Thr Arg Lys

1250

1255

1260

Asp Glu Ala Asp Ser
265

<210> 63

<211> 2105

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(1947)

<400> 63

atg aat aca gat aaa atg acc aag atg gat cta acg ggg tcc aat aac	48
Met Asn Thr Asp Lys Met Thr Lys Met Asp Leu Thr Gly Ser Asn Asn	
1 5 10 15	
gtg ccc att aat cca ccg acc act aag cgt gat ctt aga cag aat gat	96
Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp	
20 25 30	
aat aat aac cct aag agt cat aat agt cat aat agc aat ggg atg act	144
Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr	
35 40 45	
ggt aac agg aac aat aat aat aaa aat gcc ggc gga gtt gaa act agt	192
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser	
50 55 60	
aaa aaa gcg cgc tca cga ctg gaa aca cat ccc cga gat aat gag aat	240
Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn	
65 70 75 80	
aat tac aga cta gct aca agt gcc ggt acg aaa gga ggt gcg cga acc	288
Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr	
85 90 95	
gtt gac gta cca gtc ata tta agt acc cgg gaa tca caa ggc aca cgt	336
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg	
100 105 110	
tca gta aat gca aca agt aaa att aga tgc ccg gat tcc act gca att	384
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile	
115 120 125	
tgc gag tgg ttc gcc acg ccc acg gat cct caa aga cca gga gtt tat	432
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr	
130 135 140	
aac cac aag aac ggc gac aaa aac aac aga gat acc ggg aac att aat	480
Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn	
145 150 155 160	

acc gtt agc agt cta atg gat aat gct agg ggt ccg aac ccg cga tct	528
Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
165 170 175	
ggg att tca ata ccg aca cca acc tct aga caa tcc cca agt gag aca	576
Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
180 185 190	
cct cca gat cca ctg cag aat cct aat aat tat act agg tat cat aat	624
Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
195 200 205	
gat aaa aac agc aag aat agt aac aga aac tac aat aag aga aat aag	672
Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys	
210 215 220	
aac tcg acg acc ttt aat aac tcg gac ctt cct ggt cat aat aga agc	720
Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser	
225 230 235 240	
tcc cct gcg att aat gca gta aaa tca gca tca aat cga tca tct gct	768
Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
245 250 255	
ata ggt agt cga aac agt gat tta aac aat gct gct aat gat gaa cgc	816
Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
260 265 270	
cat tac gct aga tcg gga aca tat cag ata aac gct gta aca gta ctt	864
His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
275 280 285	
aga gta tta gga aga gga gca cgg cgt gat gta aag tca gca tat cat	912
Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
290 295 300	
ggc acc tgt ggt aca ggt ccc cgg atg aaa gtg ata aca ttg gct gtt	960
Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val	
305 310 315 320	
caa gag aat att aga aac cga att ata ttg gag cta cgg aca tta cac	1008
Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
325 330 335	
aag acc tct tat caa tat atc gtt ccg tat tat gat ggg atc tat aca	1056
Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
340 345 350	
gag ggc tca att ttc att cgg atg gtg gaa ctt gga tgg gta acg aat	1104
Glu Gly Ser Ile Phe Ile Arg Met Val Glu Leu Gly Trp Val Thr Asn	
355 360 365	
atc atg aac aaa acg gcg acc ata cgt gcg ccg gtt ttg ggt acg atg	1152
Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met	
370 375 380	
gca ttt cta gtg tta caa ggt cgg att tac gtt cac aga aag ttc gat	1200

Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp	
385 390 395 400	
aaa tgc ccg agc aag cgt gat ata aaa cct tca gat att ctg gta aac	1248
Lys Cys Pro Ser Lys Arg Asp Ile Lys Pro Ser Asp Ile Leu Val Asn	
405 410 415	
aat gaa ggt cga gca aag atc gca ggt ttc ggt gta agc gga cag tta	1296
Asn Glu Gly Arg Ala Lys Ile Ala Gly Phe Gly Val Ser Gly Gln Leu	
420 425 430	
caa cat act ctc tca aag gat gta act tcg gtg gag tct cct gaa cgt	1344
Gln His Thr Leu Ser Lys Asp Val Thr Ser Val Glu Ser Pro Glu Arg	
435 440 445	
cgt agt ggt agg tct tat ggt ttc gat cga gat att tgg agt gat ggt	1392
Arg Ser Gly Arg Ser Tyr Gly Phe Asp Arg Asp Ile Trp Ser Asp Gly	
450 455 460	
ata aca cgt gta tca tgc gca atc ggg aga ttc cct tat gct tgt aat	1440
Ile Thr Arg Val Ser Cys Ala Ile Gly Arg Phe Pro Tyr Ala Cys Asn	
465 470 475 480	
tac cca caa cag ctc cca caa gca tca caa cac cag cta cag caa cag	1488
Tyr Pro Gln Gln Leu Pro Gln Ala Ser Gln His Gln Leu Gln Gln Gln	
485 490 495	
caa caa aaa cga ccg gcg tta caa cca aag caa gaa caa ccg gaa gta	1536
Gln Gln Lys Arg Pro Ala Leu Gln Pro Lys Gln Glu Gln Pro Glu Val	
500 505 510	
gag aaa cac cga tta caa ata cca cgt caa aat tta gct gta tat aat	1584
Glu Lys His Arg Leu Gln Ile Pro Arg Gln Asn Leu Ala Val Tyr Asn	
515 520 525	
agt aat cac gat ata tgg aat aat cgc aat aga gat aaa tat att att	1632
Ser Asn His Asp Ile Trp Asn Asn Arg Asn Arg Asp Lys Tyr Ile Ile	
530 535 540	
agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat	1680
Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp	
545 550 555 560	
cta agc agt ggc gag tta ggt gaa agt cgt gag gtt gtg cca gac ggt	1728
Leu Ser Ser Gly Glu Leu Gly Glu Ser Arg Glu Val Val Pro Asp Gly	
565 570 575	
atc ggg ttg gag gta ctt cta gat tct atc gta aaa gaa gag gta cga	1776
Ile Gly Leu Glu Val Leu Leu Asp Ser Ile Val Lys Glu Glu Val Arg	
580 585 590	
atg gaa cca tca aca gtt tcg aag gaa ttt agg tcg atc att tct gaa	1824
Met Glu Pro Ser Thr Val Ser Lys Glu Phe Arg Ser Ile Ile Ser Glu	
595 600 605	
tgt tta cga aac gat gca act gaa aga caa aca gct tca aac tta gta	1872
Cys Leu Arg Asn Asp Ala Thr Glu Arg Gln Thr Ala Ser Asn Leu Val	

610 615 620
 aat cac gaa ttt gta aag aaa tat caa aag tac aat cgt gaa aaa tgg 1920
 Asn His Glu Phe Val Lys Lys Tyr Gln Lys Tyr Asn Arg Glu Lys Trp
 625 630 635 640
 acc gca gat tta caa agg tgg caa taa aaatcgctt cagcctgat 1967
 Thr Ala Asp Leu Gln Arg Trp Gln
 645
 cgctgacgct cgacgcctgc ccccgacctg cagctcgccc agctcgccca ggctcgccca 2027
 gcctgcccac cagcctgccc caccgctcca cgctaaata ataaaaattt ttaaaaaaaaa 2087
 aaaaaaaaaa aaaccgct 2105

 <210> 64
 <211> 648
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 64
 Met Asn Thr Asp Lys Met Thr Lys Met Asp Leu Thr Gly Ser Asn Asn
 1 5 10 15
 Val Pro Ile Asn Pro Pro Thr Thr Lys Arg Asp Leu Arg Gln Asn Asp
 20 25 30
 Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr
 35 40 45
 Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser
 50 55 60
 Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
 65 70 75 80
 Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
 85 90 95
 Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
 100 105 110
 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
 115 120 125
 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
 130 135 140
 Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
 145 150 155 160
 Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
 165 170 175
 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

139

<400>	65
acacagttat tggccgctcgg attca atg gaa gga tta gct atc aga gca tct Met Glu Gly Leu Ala Ile Arg Ala Ser	52
1 5	
cga ccg tcg gtt ttc tgt tct att cca ggt ctg gcc gcc gat tcc cac Arg Pro Ser Val Phe Cys Ser Ile Pro Gly Leu Gly Gly Asp Ser His	100
10 15 20 25	
cga aaa cct cca agt gac ggt ttc ctg aag ctg cct gcg tcg tct att Arg Lys Pro Pro Ser Asp Gly Phe Leu Lys Leu Pro Ala Ser Ser Ile	148
30 35 40	
ccg gcg gac agc cga aaa tta gta gcg aat tct act tcc ttt cat cca	196

Pro	Ala	Asp	Ser	Arg	Lys	Leu	Val	Ala	Asn	Ser	Thr	Ser	Phe	His	Pro	
			45					50					55			
atc	tca	gcc	gtt	aac	gtc	tct	gct	caa	gct	tcc	ctc	acc	gct	gat	ttt	244
Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
		60					65				70					
ccc	gcc	ctt	tca	gaa	act	ata	ctg	aaa	gag	gga	aga	aat	aac	gga	aaa	292
Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
		75				80				85						
gag	aaa	gca	gag	aac	atc	gtg	tgg	cac	gag	agt	tcg	ata	tgc	aga	tgc	340
Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys	
	90				95				100						105	
gac	aga	caa	caa	ctt	ctt	caa	caa	aag	ggg	tgt	gtc	gtt	tgg	atc	act	388
Asp	Arg	Gln	Gln	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr		
			110					115					120			
ggg	ctc	agt	ggg	tca	ggg	aaa	agc	act	gtt	gct	tgt	gca	cta	agt	aaa	436
Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Cys	Ala	Leu	Ser	Lys	
			125					130					135			
gca	ttg	ttt	gaa	aga	ggc	aaa	ctt	act	tac	aca	ctc	gac	ggc	gac	aat	484
Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
		140					145					150				
gtc	cgt	cac	ggc	ctt	aac	cgt	gac	ctc	act	ttc	aaa	gca	gag	cac	cgc	532
Val	Arg	His	Gly	Leu	Asn	Arg	Asp	Leu	Thr	Phe	Lys	Ala	Glu	His	Arg	
		155				160					165					
acc	gaa	aac	att	aga	aga	att	ggg	gag	gtg	gct	aag	ttg	ttt	gct	gac	580
Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp	
	170				175				180						185	
gtc	gga	gtc	att	tgt	ata	gca	agt	ttg	att	tct	ccg	tac	cgg	aga	gac	628
Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
			190						195					200		
aga	gac	gcg	tgc	cgg	tcc	ttg	tta	cct	gac	ggc	gat	ttc	gtc	gag	gtc	676
Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val	
			205					210					215			
ttc	atg	gac	gtt	cct	ctt	cat	gtg	tgc	gag	tcg	aga	gat	cca	aag	ggg	724
Phe	Met	Asp	Val	Pro	Leu	His	Val	Cys	Glu	Ser	Arg	Asp	Pro	Lys	Gly	
		220					225					230				
ttg	tac	aag	ctt	gca	cgt	gca	ggc	aaa	atc	aaa	ggc	ttc	act	gga	atc	772
Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
		235				240					245					
gac	gac	cct	tac	gag	gca	cca	gtg	aat	tgc	gag	gta	gtg	ctg	aaa	cac	820
Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His	
		250			255				260						265	
aca	gga	gac	gac	gag	tcg	tgt	tcg	cca	cgt	cag	atg	gct	gag	aac	atc	868
Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile	

270 275 280
 atc tct tac ctg caa aac aaa ggt tat ctt gag ggc taa gtcaaaagtcg 917
 Ile Ser Tyr Leu Gln Asn Lys Gly Tyr Leu Glu Gly
 285 290

 gaa 920

 <210> 66
 <211> 293
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 66
 Met Glu Gly Leu Ala Ile Arg Ala Ser Arg Pro Ser Val Phe Cys Ser
 1 5 10 15
 Ile Pro Gly Leu Gly Gly Asp Ser His Arg Lys Pro Pro Ser Asp Gly
 20 25 30
 Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
 35 40 45
 Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
 50 55 60
 Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
 65 70 75 80
 Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
 85 90 95
 Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
 100 105 110
 Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
 115 120 125
 Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
 130 135 140
 Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
 145 150 155 160
 Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
 165 170 175
 Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
 180 185 190
 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
 195 200 205
 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
 210 215 220

Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
225 230 235 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro
245 250 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys
260 265 270

Ser Pro Arg Gln Met Ala Glu Asn Ile Ile Ser Tyr Leu Gln Asn Lys
275 280 285

Gly Tyr Leu Glu Gly
290

<210> 67

<211> 1257

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (13)..(1245)

<400> 67

aattactcaa tc atg ggg att tgc ttg agt gct cag gtc aaa gct gag agc 51
Met Gly Ile Cys Leu Ser Ala Gln Val Lys Ala Glu Ser
1 5 10

tca gga gcg agt acg aag tat gac gcc aaa gat ata gga agt ctt ggg 99
Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly
15 20 25

agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt 147
Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly
30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195
Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu
50 55 60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243
Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291
Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr
80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339
Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387
Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

110	115	120	125	
ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc				435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys	130	135	140	
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt				483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta				531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct				723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

ctc gaa cac att cag tct tta aat gct gct ata gga gga aat atg gat 1107
 Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
 350 355 360 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
 Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
 370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
 Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
 385 390 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
 Val Ala Tyr Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val
 400 405 410

atagggttaa ac 1257

<210> 68
 <211> 410
 <212> PRT
 <213> Arabidopsis thaliana

<400> 68
 Met Gly Ile Cys Leu Ser Ala Gln Val Lys Ala Glu Ser Ser Gly Ala
 1 5 10 15

Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly Ser Lys Ala
 20 25 30

Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly Glu Ile Leu
 35 40 45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
 50 55 60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
 85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
 100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
 115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
 130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
 145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

165										170					175				
Leu	Arg	Leu	Lys	Val	Ala	Leu	Gly	Ala	Ala	Lys	Gly	Leu	Ala	Phe	Leu				
			180					185					190						
His	Ser	Ser	Glu	Thr	Arg	Val	Ile	Tyr	Arg	Asp	Phe	Lys	Thr	Ser	Asn				
		195					200					205							
Ile	Leu	Leu	Asp	Ser	Glu	Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu				
	210					215					220								
Ala	Lys	Asp	Gly	Pro	Ile	Gly	Asp	Lys	Ser	His	Val	Ser	Thr	Arg	Val				
225					230					235					240				
Met	Gly	Thr	His	Gly	Tyr	Ala	Ala	Pro	Glu	Tyr	Leu	Ala	Thr	Gly	His				
			245					250						255					
Leu	Thr	Thr	Lys	Ser	Asp	Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu				
			260					265					270						
Leu	Leu	Ser	Gly	Arg	Arg	Ala	Val	Asp	Lys	Asn	Arg	Pro	Ser	Gly	Glu				
		275					280					285							
Arg	Asn	Leu	Val	Glu	Trp	Ala	Lys	Pro	Tyr	Leu	Val	Asn	Lys	Arg	Lys				
	290					295					300								
Ile	Phe	Arg	Val	Ile	Asp	Asn	Arg	Leu	Gln	Asp	Gln	Tyr	Ser	Met	Glu				
305				310					315					320					
Glu	Ala	Cys	Lys	Val	Ala	Thr	Leu	Ser	Leu	Arg	Cys	Leu	Thr	Thr	Glu				
			325					330					335						
Ile	Lys	Leu	Arg	Pro	Asn	Met	Ser	Glu	Val	Val	Ser	His	Leu	Glu	His				
		340					345						350						
Ile	Gln	Ser	Leu	Asn	Ala	Ala	Ile	Gly	Gly	Asn	Met	Asp	Lys	Thr	Asp				
	355						360					365							
Arg	Arg	Met	Arg	Arg	Arg	Ser	Asp	Ser	Val	Val	Ser	Lys	Lys	Val	Asn				
	370					375					380								
Ala	Gly	Phe	Ala	Arg	Gln	Thr	Ala	Val	Gly	Ser	Thr	Val	Val	Ala	Tyr				
385				390					395					400					
Pro	Arg	Pro	Ser	Ala	Ser	Pro	Leu	Tyr	Val										
			405					410											

<210> 69
 <211> 3240
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (69)..(236)

<220>
 <221> CDS
 <222> (420) .. (506)

<220>
 <221> CDS
 <222> (581) .. (822)

<220>
 <221> CDS
 <222> (907) .. (1126)

<220>
 <221> CDS
 <222> (1276) .. (1355)

<220>
 <221> CDS
 <222> (1442) .. (1526)

<220>
 <221> CDS
 <222> (1684) .. (1815)

<220>
 <221> CDS
 <222> (1911) .. (2024)

<220>
 <221> CDS
 <222> (2196) .. (2243)

<220>
 <221> CDS
 <222> (2734) .. (2818)

<220>
 <221> CDS
 <222> (2928) .. (2984)

<220>
 <221> CDS
 <222> (3079) .. (3191)

<400> 69
 ctttcgtgtg aacttcggtc catatcctta gctctttgtt tggtatttac atttcataca 60

gacgcaaa atg cta gag aaa aaa tta gct gct gca gaa gtc tct gag gaa 110
 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
 1 5 10

gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
 15 20 25 30

atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

Met Arg Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu
35 40 45

aca atg att ggg aag ggt gca ttc gga gag gtaacatctc ttttatagat 256
Thr Met Ile Gly Lys Gly Ala Phe Gly Glu
50 55

catagtctgt tactctgttt tctcagcctc tcattggcat gcacatcttt gaaatgttct 316

ctgtgatgca tccttcttga aaggctcttct taggccattt tttttaccac agctaatttt 376

tcaaaaaagt atggcatgct aatttttctc tttctctttg cag gtt agg atc tgt 431
Val Arg Ile Cys
60

agg gag aag gga aca ggc aat gtc tat gca atg aag aag ctt aag aaa 479
Arg Glu Lys Gly Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys
65 70 75

tct gag atg ctt cgc aga ggc cag gta tttaaattcc ttcaagtggc 526
Ser Glu Met Leu Arg Arg Gly Gln Val
80 85

tttcgtttga catttgttta gttggttgat gtgaatgtgg aatctgattt tcag gtg 583
Val

gaa cat gta aaa gca gag aga aat tta ctt gca gaa gtt gat agc aat 631
Glu His Val Lys Ala Glu Arg Asn Leu Leu Ala Glu Val Asp Ser Asn
90 95 100

tgc att gtc aaa ctg tat tgt tct ttc caa gat gaa gag tac ttg tat 679
Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln Asp Glu Glu Tyr Leu Tyr
105 110 115

ctc ata atg gag tat tta cct ggt ggg gat atg atg act tta ctt atg 727
Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp Met Met Thr Leu Leu Met
120 125 130

agg aaa gac acc ctc act gaa gac gag gcc agg ttt tat att ggg gaa 775
Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala Arg Phe Tyr Ile Gly Glu
135 140 145 150

act gtc ctg gct att gag tcc att cat aag cac aac tac att cac ag 822
Thr Val Leu Ala Ile Glu Ser Ile His Lys His Asn Tyr Ile His Ar
155 160 165

gtcagtgaa gagaatatat gatttagttc tagctcccat tggtattttg ttctaaacgt 882

ctttttttct ccaatgtgat acag a gat atc aag cct gat aat ctg cta ctt 934
g Asp Ile Lys Pro Asp Asn Leu Leu Leu
s 170 175

gac aaa gac ggc cac atg aaa ttg tca gat ttt gga tta tgt aaa cca 982
Asp Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro
180 185 190

tta gac tgt agt aat ctt caa gag aaa gac ttt aca gtt gca aga aac 1030

Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
 195 200 205
 gtt agt ggg gct tta caa agt gat ggt cgc cct gtg gcg aca aga cgc 1078
 Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg
 210 215 220
 acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt 1126
 Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
 225 230 235
 gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186
 gtatatttcg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246
 acttactagg ttaaggtcat tactttcag gct tat tcc aca gtt ggc act cct 1299
 Ala Tyr Ser Thr Val Gly Thr Pro
 240 245
 gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa 1347
 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
 250 255 260
 tgt gat tg gtaggtgaag ccaacctatt cctatttgtg gtctttgatt tctttggtgt 1405
 Cys Asp Tr
 265
 aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460
 p Trp Ser Leu Gly Ala Ile
 270
 atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca 1508
 Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
 275 280 285
 atg aca act tgt agg aag gtaattaac cattcctttt tgaatctttc 1556
 Met Thr Thr Cys Arg Lys
 290
 attttaatat tgaaggcaga ctggcgattt caagtcttac atttaatttt agtctttttg 1616
 tatctctttg gtaattctaa tgtggaaact tacctcttct cgattcatta tcttccccct 1676
 tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt 1725
 Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
 295 300 305
 aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773
 Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
 310 315 320
 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815
 Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
 325 330 335
 gtgtgtgatg cgttgttcaa ctttgagatt caaagttccc ttatgtaaga tcattgtgtg 1875

150

```

<400> 70
Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu Glu Gln
  1          5          10          15
Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr Met Arg
      20          25          30
Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu Thr Met
      35          40          45
Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly
   50          55          60
Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys Ser Glu Met Leu
  65          70          75          80
Arg Arg Gly Gln Val Val Glu His Val Lys Ala Glu Arg Asn Leu Leu
      85          90          95
Ala Glu Val Asp Ser Asn Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln
      100          105          110
Asp Glu Glu Tyr Leu Tyr Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp
      115          120          125
Met Met Thr Leu Leu Met Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala
   130          135          140
Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys
  145          150          155          160
His Asn Tyr Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp
      165          170          175
Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu

```

152

<210> 71
 <211> 979
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (28) .. (843)

<400> 71

```

acgaaaacca ccgtagcta taggctg atg ata tgt agg atc cga ctc ggg tcg 54
                               Met Ile Cys Arg Ile Arg Leu Gly Ser
                               1           5

atg aac ggt gac gaa tgc gcg aac gtt gcg acg tgc tgg gtt act tct 102
Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
10           15           20           25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
30           35           40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
45           50           55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
60           65           70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
75           80           85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
90           95           100          105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
110          115          120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
125          130          135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
140          145          150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
155          160          165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

```

```

170          175          180          185
aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag 630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
190          195          200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
205          210          215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
220          225          230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
235          240          245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250          255          260          265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gcctttcgct 933

ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aaatca 979

```

<210> 72
 <211> 271
 <212> PRT
 <213> Arabidopsis thaliana

```

<400> 72
Met Ile Cys Arg Ile Arg Leu Gly Ser Met Asn Gly Asp Glu Cys Ala
 1          5          10          15

Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
20          25          30

Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
35          40          45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
50          55          60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
65          70          75          80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
85          90          95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
100          105          110

```

Glu Lys His Thr Arg Asp Val Glu Ala Val Arg Phe Ser Pro Arg Asp
 115 120 125
 Arg Leu Ile Val Ser Ala Gly Ala Asp Gly Val Ile Ala Val Cys Pro
 130 135 140
 Val Ala Gly Glu Cys Asp Asp Asp Ala Arg Asp Gly His Glu Asp
 145 150 155 160
 Cys Val Ser Ser Ile Cys Phe Ser Pro Ser Leu Glu His Pro Ile Leu
 165 170 175
 Phe Ser Gly Ser Cys Ile Tyr Phe Ile Lys Val Trp Asn Val Asn Gly
 180 185 190
 Lys Lys Cys Arg Thr Pro Leu Lys Lys His Ser Asn Pro Val Ser Thr
 195 200 205
 Arg Thr Gln Ser Glu Glu Gly Arg Leu Cys Ala Lys Gly Gly Lys Ser
 210 215 220
 Gly Ala Arg Leu Leu Pro Asp Leu Ser Thr Gln Glu Gln Leu Pro Lys
 225 230 235 240
 Ile Asn Gln Glu Asn Pro Ile Asn Gln Ile Ala Phe Ser Pro Ser Pro
 245 250 255
 Phe Val Val Thr Cys Gln Thr Glu Arg Ser Leu Ser Gln Thr Trp
 260 265 270

<210> 73
 <211> 1260
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (101)..(155)

<220>
 <221> CDS
 <222> (254)..(660)

<220>
 <221> CDS
 <222> (750)..(1193)

<400> 73
 gctcaattat gtttacaaca ttgttgtaat ttcaaaactt cataagaatt tctctgataa 60
 taaagaaaaa gctggagtag aactatttta aagtgtcatc atg aag aga cta agc 115
 Met Lys Arg Leu Ser
 1 5

agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
 Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
 10 15

ccattcttgt tctttctact ttttgcta gtcagacaaa acccatgtga tcctttcttc 225
 actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
 sp Ser Phe Gly Tyr Thr Thr Asp Glu
 20 25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
 Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
 30 35 40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
 Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
 45 50 55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
 His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
 60 65 70 75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
 Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
 80 85 90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
 Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
 95 100 105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
 Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
 110 115 120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
 Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
 125 130 135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
 Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu
 140 145 150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgacag att agt aaa atc aaa gct aag gta 773
 Ile Ser Lys Ile Lys Ala Lys Val
 155 160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
 Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
 165 170 175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
 Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
 180 185 190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
 195 200 205 210

gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965
 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser
 215 220 225

tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
 230 235 240

gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
 245 250 255

tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109
 Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu
 260 265 270

agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
 275 280 285 290

ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
 295 300

tcaaattggt gctctgttta gtctcaatgg gaaaacagag aagagggcaa aggtgga 1260

<210> 74

<211> 301

<212> PRT

<213> Arabidopsis thaliana

<400> 74

Met Lys Arg Leu Ser Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr
 1 5 10 15

Ser Thr Asp Ser Phe Gly Tyr Thr Thr Asp Glu Gln Ser Pro Arg Gly
 20 25 30

Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
 35 40 45

Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
 50 55 60

Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
 65 70 75 80

Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
 85 90 95

Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
 100 105 110

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
 115 120 125
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
 130 135 140
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
 145 150 155 160
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Lys Ala Ile Thr Glu
 165 170 175
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
 180 185 190
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
 195 200 205
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
 210 215 220
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
 225 230 235 240
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
 245 250 255
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
 260 265 270
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
 275 280 285
 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
 290 295 300

<210> 75
 <211> 1122
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (22)..(1122)

<400> 75
 acgtagctaa agtcggtttg a atg aac caa cgt gct gac cgt gac cgt gct 51
 Met Asn Gln Arg Ala Asp Arg Asp Arg Ala
 1 5 10
 agc tcg atc cgt tgg ttt gcc aac cga tta gtg agt ggt agc ctg tta 99
 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
 15 20 25
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala	
30 35 40	
tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
45 50 55	
gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
tat aga ctt gca cgc ctc gat aac cgc gct ctt gca caa ttg ttg cac	291
Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tcg aaa tta gag gcg	579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

255	260	265	
atc gaa tcc cgt ctc tcg acc gac gga gta ttc agc ttc tcg gta aac			867
Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn			
270	275	280	
gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga			915
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly			
285	290	295	
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att			963
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile			
300	305	310	
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc			1011
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr			
315	320	325	330
gct gac cgc cga cgc tgc gct agc ctg agc ctg ccc agc ctg cca gct			1059
Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala			
335	340	345	
cga cag ccc tcc caa acg gag aaa cgc att gtc gag aat att aag tac			1107
Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr			
350	355	360	
ggg gca gcg cca tga			1122
Gly Ala Ala Pro			
365			

<210> 76

<211> 366

<212> PRT

<213> Arabidopsis thaliana

<400> 76

Met Asn Gln Arg Ala Asp Arg Asp Arg Ala Ser Ser Ile Arg Trp Phe			
1	5	10	15
Ala Asn Arg Leu Val Ser Gly Ser Leu Leu Leu Cys Ala Asn Ala Tyr			
20	25	30	
Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala Leu Gln Gln Met Asn Arg			
35	40	45	
Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser			
50	55	60	
Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu			
65	70	75	80
Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu			
85	90	95	
Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu			
100	105	110	

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu
 115 120 125
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu
 130 135 140
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val
 145 150 155 160
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp
 165 170 175
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp
 180 185 190
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val
 195 200 205
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu
 210 215 220
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu
 225 230 235 240
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg
 245 250 255
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser
 260 265 270
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro
 275 280 285
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg
 290 295 300
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro
 305 310 315 320
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys
 325 330 335
 Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala Arg Gln Pro Ser Gln Thr
 340 345 350
 Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr Gly Ala Ala Pro
 355 360 365

<210> 77
 <211> 1650
 <212> DNA
 <213> Arabidopsis thaliana

<220>

<221> CDS
 <222> (21)..(203)

<220>
 <221> CDS
 <222> (291)..(482)

<220>
 <221> CDS
 <222> (633)..(838)

<220>
 <221> CDS
 <222> (1044)..(1605)

<400> 77

```

attcagagaa gaactcaccg atg agt atg gat ttt tca cct ttg tta acg gtt 53
      Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val
      1             5             10

ctt gag gga gat ttc aac aag gat aat act tct tct gca aca gaa att 101
Leu Glu Gly Asp Phe Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile
      15             20             25

gat act tta gag aac tta gat gac act agg cag ata agt aaa gga aaa 149
Asp Thr Leu Glu Asn Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys
      30             35             40

cct ccg agg cac ctc aca agc agt gct act agg ctg cag ctt gca gcc 197
Pro Pro Arg His Leu Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala
      45             50             55

aat gcg gtaatatact tgaccctgct ttttcttttt ccttttcttt gttacaatgg 253
Asn Ala
      60

gattcgaatg atgtaactgg tttctgtttg tgcgcag gat gtg gat gtt tgt aac 308
      Asp Val Asp Val Cys Asn
      65

ttg gtt atg aag tca ctt gat gac aaa tca gag ttt cta cct gta tac 356
Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu Pro Val Tyr
      70             75             80

cga tca gga agt tgt gct gag caa ggg gca aaa cag ttc atg gaa gat 404
Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe Met Glu Asp
      85             90             95

gaa cac att tgc atc gat gat ctt gtt aat cat ctt ggt gca gct att 452
Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly Ala Ala Ile
100             105             110             115

caa tgc tct tct ctt gga gcc ttc tat ggg gtgagtttat cttccaatct 502
Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly
      120             125

tacccaaaga agcataaaag caattcacta gcctgattct tctttcttct cctcttttgt 562

```

actagtacga tataagaggt attacttcaa aaactcttct aacatttggt gattgtgtgt 622

cctttggcag gta ttt gat ggc cac ggt ggc aca gat gca gca cac ttt 671
Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719
Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767
Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815
Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Ala
175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868
Leu Thr Ala Phe Ile Phe Gly Ar
190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044
g

agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092
Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140
Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188
Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236
Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284
Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332
Leu Glu Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380
Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
 310 315 320

gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
 325 330 335

gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
 340 345 350

cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
 355 360 365 370

cta ctc aaa gcc gtg ctc gat gcc tat ccg tga gcatgttatg ttgtacgtta 1625
 Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
 375 380

ctttgtgaga ctattgccaa gtttag 1650

<210> 78
 <211> 380
 <212> PRT
 <213> Arabidopsis thaliana

<400> 78
 Met Ser Met Asp Phe Ser Pro Leu Leu Thr Val Leu Glu Gly Asp Phe
 1 5 10 15
 Asn Lys Asp Asn Thr Ser Ser Ala Thr Glu Ile Asp Thr Leu Glu Asn
 20 25 30
 Leu Asp Asp Thr Arg Gln Ile Ser Lys Gly Lys Pro Pro Arg His Leu
 35 40 45
 Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
 50 55 60
 Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
 65 70 75 80
 Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
 85 90 95
 Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
 100 105 110
 Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
 115 120 125
 Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
 130 135 140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala
 145 150 155 160
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser
 165 170 175
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe
 180 185 190
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu
 195 200 205
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn
 210 215 220
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr
 225 230 235 240
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp
 245 250 255
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu
 260 265 270
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile
 275 280 285
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val
 290 295 300
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys
 305 310 315 320
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn
 325 330 335
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile
 340 345 350
 Glu Ile Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly
 355 360 365
 Leu Asn Leu Leu Lys Gly Val Leu Asp Gly Tyr Pro
 370 375 380

<210> 79
 <211> 589
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(575)

<400> 79


```

atctttttcc gataact atg gct gag gaa atc aag aat gtt cct gaa cag      50
      Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln
        1              5              10

gag gtg cca aag gta gca aca gag gaa tca tcg gca gag gtt aca gat      98
Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
      15              20              25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
      30              35              40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
      45              50              55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
      60              65              70              75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
      80              85              90

ggg gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
      95              100              105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
      110              115              120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
      125              130              135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
      140              145              150              155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
      160              165              170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys Asp Lys Glu
      175              180              185

gaagattatc attaa      590

```

<210> 80

<211> 185

<212> PRT

<213> Arabidopsis thaliana

<400> 80

Met Ala Glu Glu Ile Lys Asn Val Pro Glu Gln Glu Val Pro Lys Val
 1 5 10 15
 Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp Arg Gly Leu Phe Asp
 20 25 30
 Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile
 35 40 45
 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu
 50 55 60
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser
 65 70 75 80
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys
 85 90 95
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu
 100 105 110
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly
 115 120 125
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val
 130 135 140
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile
 145 150 155 160
 Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr His Pro Lys Thr Thr
 165 170 175
 Val Glu Glu Glu Lys Lys Asp Lys Glu
 180 185

<210> 81
 <211> 1376
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(1366)

<400> 81
 agcaatcgag aaaaaagca atg gcg tca gac aaa caa aag gcg gag aga gcc 52
 Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala
 1 5 10
 gag gtt gcg gcg agg cta gcg gct gag gac ttg cat gac att aac aaa 100
 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
 15 20 25
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
		30					35					40					
gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggt	gtg	ata	ggt	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
	60				65				70					75			
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
			95					100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggt	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
		110				115						120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
	125					130					135						
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
	140				145					150					155		
aag	acg	gcg	gag	aag	att	ggt	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
			160						165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
			175					180					185				
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
		190					195					200					
aag	gtt	ggt	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205					210					215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
	220				225					230				235			
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
			240						245					250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

255	260	265	
gtt gag aca gcg aag aga gct atg ggt ttc ttg tcg ggg aag aca gag Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu 270 275 280			868
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn 285 290 295			916
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg 300 305 310 315			964
ttg gaa ggt aaa gag ctg aaa gaa gaa gct gga gca aaa gcc caa gag Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu 320 325 330			1012
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala 335 340 345			1060
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly 350 355 360			1108
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys 365 370 375			1156
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu 380 385 390 395			1204
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser 400 405 410			1252
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr 415 420 425			1300
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys 430 435 440			1348
gat aag gga aag ctg tga gaatactaga Asp Lys Gly Lys Leu 445			1376

<210> 82

<211> 448

<212> PRT

<213> Arabidopsis thaliana

<400> 82

Met Ala Ser Asp Lys Gln Lys Ala Glu Arg Ala Glu Val Ala Ala Arg
 1 5 10 15
 Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys Ser Gly Gly Ala Asp
 20 25 30
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu
 35 40 45
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly
 50 55 60
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala
 65 70 75 80
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val
 85 90 95
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr
 100 105 110
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala
 115 120 125
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn
 130 135 140
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys
 145 150 155 160
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys
 165 170 175
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp
 180 185 190
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr
 195 200 205
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala
 210 215 220
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu
 225 230 235 240
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr
 245 250 255
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys
 260 265 270
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys
 275 280 285
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu
 305 310 315 320
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr
 325 330 335
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp
 340 345 350
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala
 355 360 365
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser
 370 375 380
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly
 385 390 395 400
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val
 405 410 415
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn
 420 425 430
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu
 435 440 445

<210> 83
 <211> 561
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (18)..(548)

<400> 83
 aaccacacaa atacaaa atg aat gaa atg tcg ttc ttt ggt tat agt ttc 50
 Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe
 1 5 10
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr
 15 20 25
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln
 30 35 40
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly
 45 50 55
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggt caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84

<211> 176

<212> PRT

<213> Arabidopsis thaliana

<400> 84

Met Asn Glu Met Ser Phe Phe Gly Tyr Ser Phe Ile Val Val Ala Leu	1	5	10	15
Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr Pro Ala Gln Pro Pro	20	25	30	
Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val	35	40	45	
His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn	50	55	60	
Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg	65	70	75	80
Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala	85	90	95	
Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met	100	105	110	

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
 115 120 125

Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
 130 135 140

Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
 145 150 155 160

Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
 165 170 175

<210> 85
 <211> 988
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(977)

<400> 85
 tttttaagaa a atg gca gct tct aag cga cta gtt gtc tct tgc ttg ttc 50
 Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe
 1 5 10

tta gtt ttg ttg ttt gct caa gcc aat tgc caa ggt ttg aaa gta ggt 98
 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
 15 20 25

ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
 30 35 40 45

gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
 50 55 60

aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
 65 70 75

ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
 80 85 90

cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
 95 100 105

gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
 110 115 120 125

gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt 434
 Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val
 130 135 140

gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac 482
 Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn
 145 150 155

ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc 530
 Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg
 160 165 170

tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac 578
 Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His
 175 180 185

aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac 626
 Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn
 190 195 200 205

ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc 674
 Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala
 210 215 220

gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta 722
 Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu
 225 230 235

gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg 770
 Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr
 240 245 250

cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc 818
 Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu
 255 260 265

gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat 866
 Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His
 270 275 280 285

ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt 914
 Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly
 290 295 300

cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt 962
 Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys
 305 310 315

cgg tct gct aat taa gagatataga aa 989
 Arg Ser Ala Asn
 320

<210> 86

<211> 321

<212> PRT

<213> Arabidopsis thaliana

<400> 86

Met Ala Ala Ser Lys Arg Leu Val Val Ser Cys Leu Phe Leu Val Leu
 1 5 10 15
 Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly Phe Tyr Ser
 20 25 30
 Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val Val Phe Asp
 35 40 45
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
 50 55 60
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
 65 70 75 80
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
 85 90 95
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
 100 105 110
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
 115 120 125
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
 130 135 140
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
 145 150 155 160
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
 165 170 175
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
 180 185 190
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
 195 200 205
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
 210 215 220
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
 225 230 235 240
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
 245 250 255
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
 260 265 270
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
 275 280 285
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

290 295 300
 Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
 305 310 315 320

Asn

<210> 87
 <211> 650
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (8) .. (634)

<400> 87
 agcgaca atg gcg tcg att acg aac ctc gcc tct tct ctc tct tca ctc 49
 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu
 1 5 10
 tcg ttc tcc tcc caa gtt tct caa aga cct aac acc att tcc ttc ccc 97
 Ser Phe Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro
 15 20 25 30
 cgc gcg aat tca gta ttc gca tta ccg gcg aaa tcc gca cgc cgc gct 145
 Arg Ala Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala
 35 40 45
 tct cta tct atc acc gcc acg gta tct gct cca ccg gag gag gag gag 193
 Ser Leu Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu
 50 55 60
 ata gtt gaa ctg aag aaa tac gtc aaa tcg agg ctt ccc gga gga ttt 241
 Ile Val Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe
 65 70 75
 gct gct cag aag att att ggc act gga cga cgt aag tgc gca atc gct 289
 Ala Ala Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala
 80 85 90
 aga gtt gtt ctt cag gaa ggt act ggg aag gtt atc atc aac tat cgt 337
 Arg Val Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg
 95 100 105 110
 gat gcc aag gag tac ctt cag gga aat cca ttg tgg ctt cag tat gtt 385
 Asp Ala Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val
 115 120 125
 aaa gta cca ttg gtg act tta gga tat gag aat agc tac gac ata ttt 433
 Lys Val Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe
 130 135 140
 gtg aaa gcc cat gga ggc ggt ctc tca ggt caa gct caa gca att acc 481
 Val Lys Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr

145 150 155
 ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg 529
 Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser
 160 165 170
 cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa 577
 Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu
 175 180 185 190
 aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc 625
 Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser
 195 200 205
 aag cgt taa gagttttata tatcat 650
 Lys Arg

 <210> 88
 <211> 208
 <212> PRT
 <213> Arabidopsis thaliana

 <400> 88
 Met Ala Ser Ile Thr Asn Leu Ala Ser Ser Leu Ser Ser Leu Ser Phe
 1 5 10 15
 Ser Ser Gln Val Ser Gln Arg Pro Asn Thr Ile Ser Phe Pro Arg Ala
 20 25 30
 Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu
 35 40 45
 Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val
 50 55 60
 Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala
 65 70 75 80
 Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val
 85 90 95
 Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala
 100 105 110
 Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val
 115 120 125
 Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys
 130 135 140
 Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly
 145 150 155 160
 Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu
 165 170 175

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
 180 185 190

Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
 195 200 205

<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

aacaagtga gcaca atg ggg atc atc gaa agg att aaa gaa atc gag gcc 51
 Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala
 1 5 10

gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99
 Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
 15 20 25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147
 Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
 30 35 40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
 Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
 45 50 55 60

ggg cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243
 Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
 65 70 75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291
 Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
 80 85 90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339
 Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
 95 100 105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcc 387
 Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
 110 115 120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
 Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
 125 130 135 140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
 Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
 145 150 155

caa ata ttg act aag gaa ctt gag gca gtg ggc ttg cga cta aac aaa	531
Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
 385 390 395

ctt aag caa taa gcttttag 1223
 Leu Lys Gln
 400

<210> 90

<211> 399

<212> PRT

<213> Arabidopsis thaliana

<400> 90

Met Gly Ile Ile Glu Arg Ile Lys Glu Ile Glu Ala Glu Met Ala Arg
 1 5 10 15

Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala
 20 25 30

Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
 35 40 45

Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
 50 55 60

Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
 65 70 75 80

Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
 85 90 95

Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
 100 105 110

Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
 115 120 125

Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
 130 135 140

Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
 145 150 155 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
 165 170 175

Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
 180 185 190

Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
 195 200 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
 225 230 235 240
 Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
 245 250 255
 Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
 260 265 270
 Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
 275 280 285
 Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
 290 295 300
 Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
 305 310 315 320
 Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
 325 330 335
 Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
 340 345 350
 Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
 355 360 365
 Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
 370 375 380
 Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
 385 390 395

<210> 91
 <211> 536
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(524)

<400> 91
 aaataaaaac a atg aca agc tcc gat caa tct cca tcg cac gac gtc ttc 50
 Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe
 1 5 10
 gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98
 Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
 15 20 25
 tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146
 Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
 30 35 40 45

aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
 Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
 50 55 60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
 Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
 65 70 75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
 Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
 80 85 90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
 Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
 95 100 105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
 Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
 110 115 120 125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
 Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
 130 135 140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
 Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
 145 150 155

gag aag ttt gta caa gat gat tct tct ccg gct tgc gct tga 524
 Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
 160 165 170

agaagttgtt ta 536

<210> 92

<211> 170

<212> PRT

<213> Arabidopsis thaliana

<400> 92

Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe Val Tyr Gly
 1 5 10 15

Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
 20 25 30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
 35 40 45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
 50 55 60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
 65 70 75 80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

85 90 95
 Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val Trp Ala Asn
 100 105 110
 Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu Glu Trp Lys
 115 120 125
 Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys Phe Met Glu
 130 135 140
 Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe Glu Lys Phe
 145 150 155 160
 Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
 165 170

<210> 93
 <211> 293
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (16)..(71)
 <220>
 <221> CDS
 <222> (197)..(278)

<400> 93
 agagaagtaa gagaa atg gca ggt tct aac tgt gga tgt ggc tcc tcc tgc 51
 Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys
 1 5 10

aaa tgt ggt gat tgc tgc ag gtaaacccta gattctctct tcattaactt 101
 Lys Cys Gly Asp Ser Cys Se
 15

atcatgcata tatatcctaa tatacatgtg gttacatatt ccttaagata aattttgaaa 161

tcttatactt ctgttggttt tttggtatga caaag t tgc gag aag aac tac aac 215
 r Cys Glu Lys Asn Tyr Asn
 20 25

aag gag tgt gat aac tgt agc tgt gga tca aac tgc agc tgc ggg tca 263
 Lys Glu Cys Asp Asn Cys Ser Cys Gly Ser Asn Cys Ser Cys Gly Ser
 30 35 40

agc tgt aac tgt tga agaaattatc agcat 293
 Ser Cys Asn Cys
 45

<210> 94

<211> 45
 <212> PRT
 <213> Arabidopsis thaliana

<400> 94
 Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp
 1 5 10 15
 Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser
 20 25 30
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
 35 40 45

<210> 95
 <211> 880
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (14)..(868)

<400> 95
 cacaccaaca cca atg tct gct tct tct tta ttt aat ctc cca ttg att 49
 Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile
 1 5 10
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
 15 20 25
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
 30 35 40
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
 45 50 55 60
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
 65 70 75
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
 80 85 90
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
 95 100 105
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser
 110 115 120

aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
 Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
 125 130 135 140
 cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
 His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
 145 150 155
 gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
 Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
 160 165 170
 gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
 Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
 175 180 185
 tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
 Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
 190 195 200
 ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
 Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
 205 210 215 220
 gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
 Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
 225 230 235
 aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
 Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
 240 245 250
 aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
 Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
 255 260 265
 aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
 Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 270 275 280
 tga acatcttttt tt 880
 285

<210> 96

<211> 284

<212> PRT

<213> Arabidopsis thaliana

<400> 96

Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
 1 5 10 15

Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
 20 25 30

Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
 35 40 45
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
 50 55 60
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
 65 70 75 80
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn
 85 90 95
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 100 105 110
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
 115 120 125
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
 130 135 140
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
 145 150 155 160
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
 165 170 175
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
 180 185 190
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
 195 200 205
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
 210 215 220
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
 225 230 235 240
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
 245 250 255
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
 260 265 270
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 275 280

<210> 97
 <211> 831
 <212> DNA
 <213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18)..(821)

<400> 97

tgcaactac	aacctca	atg gcc gcc tca aca atg gct ctc tcc tcc cct	50
		Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro	
		1 5 10	
gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc	98		
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val			
	15 20 25		
ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag	146		
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys			
	30 35 40		
ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg	194		
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu			
	45 50 55		
ggt cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc	242		
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro			
	60 65 70 75		
gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca	290		
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr			
	80 85 90		
ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg	338		
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met			
	95 100 105		
ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga	386		
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly			
	110 115 120		
gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc	434		
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe			
	125 130 135		
agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct	482		
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala			
	140 145 150 155		
cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc	530		
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala			
	160 165 170		
gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag	578		
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu			
	175 180 185		
gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc	626		
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr			
	190 195 200		
gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga	674		

```

Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
205                210                215
aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc 722
Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
220                225                230                235

act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca 770
Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
240                245                250

gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag 818
Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
255                260                265

tga gccaaagtttt 831

```

<210> 98
 <211> 267
 <212> PRT
 <213> Arabidopsis thaliana

```

<400> 98
Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
1          5          10          15

Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
20          25          30

Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
35          40          45

Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
50          55          60

Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
65          70          75          80

Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
85          90          95

Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
100         105         110

Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
115         120         125

Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
130         135         140

Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
145         150         155         160

Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
165         170         175

```

Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
 260 265

<210> 99
 <211> 855
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (15)..(164)

<220>
 <221> CDS
 <222> (257)..(305)

<220>
 <221> CDS
 <222> (416)..(843)

<400> 99
 cacagtatta acaa atg gca gga atc aaa gtt ttc ggt cac cca gct tcc 50
 Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser
 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194
 Pro Phe Ile Leu Arg Asn
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att 301
 Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
 55 60 65
 ttc g gtaaatacaa atatataca ttatagtcatt gtttacaat ttttggtttt 355
 Phe G
 atgatcattg caataataga aagcagaaac actcaaaaat gttttttttt tgggtgggcag 415
 aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa 462
 lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
 70 75 80
 gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg 510
 Gly Asn Asn Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
 85 90 95
 ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt 558
 Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
 100 105 110
 gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa 606
 Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
 115 120 125
 act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt 654
 Thr Val Val Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
 130 135 140 145
 tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc 702
 Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
 150 155 160
 act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga 750
 Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
 165 170 175
 act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg 798
 Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
 180 185 190
 gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa 843
 Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
 195 200 205
 gtgaatctca aa 855

<210> 100

<211> 208

<212> PRT

<213> Arabidopsis thaliana

<400> 100

Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser Thr Ala Thr Arg
 1 5 10 15

Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp Phe Glu Phe Val
 20 25 30
 His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu
 35 40 45
 Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys
 50 55 60
 Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
 65 70 75 80
 Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
 85 90 95
 Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
 100 105 110
 Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
 115 120 125
 Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
 130 135 140
 Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
 145 150 155 160
 His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
 165 170 175
 Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
 180 185 190
 Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
 195 200 205

<210> 101
 <211> 512
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (12)..(67)

<220>
 <221> CDS
 <222> (241)..(309)

<220>
 <221> CDS
 <222> (417)..(492)

<400> 101
 tatctgaaaa a atg tca gag acc aac aag aat gcc ttc caa gcc ggt cag 50

Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
 1 5 10

acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97
 Thr Ala Gly Lys Ala Gl
 15

cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
 actagaaatt tcagttactt gtttaattta gtttgcgta attatgtaat tgatgatttt 217
 atggttacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268
 u Glu Lys Ser Asn Val Leu Leu Asp Lys
 20 25

gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gly Ala Gln Gl
 30 35 40

ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432
 n Ala Gly Lys Ser Val
 45

tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
 50 55 60

ctg aac aag tag agattcgggt caaatttggg 512
 Leu Asn Lys
 65

<210> 102
 <211> 66
 <212> PRT
 <213> Arabidopsis thaliana

<400> 102
 Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
 1 5 10 15

Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
 20 25 30

Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
 35 40 45

Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
 50 55 60

Asn Lys
 65

<210> 103
 <211> 1138
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (11)..(1123)

<400> 103
 aaaacaaaa atg gcg act ttg gtt gat cct cct aat ggg ata agg aat 49
 Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn
 1 5 10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
 15 20 25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
 30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
 50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
 65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
 80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
 95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
 110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
 130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
 145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
 160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
 175 180 185

atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
 190 195 200 205
 ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
 210 215 220
 tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
 225 230 235
 gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
 240 245 250
 aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
 255 260 265
 att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
 270 275 280 285
 ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
 290 295 300
 ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
 Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
 305 310 315
 tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
 320 325 330
 cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
 335 340 345
 gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
 350 355 360 365
 tta aac act gag ctc tga gctcaagtct tgttt 1138
 Leu Asn Thr Glu Leu
 370

<210> 104

<211> 370

<212> PRT

<213> Arabidopsis thaliana

<400> 104

Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn Glu Gly Lys

1	5	10	15
His Tyr Phe	Ser Met Trp Gln Thr Leu Phe Glu Ile Asp Thr Lys Tyr		
	20	25	30
Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser			
	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His			
	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu			
	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp			
	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val			
	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln			
	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg			
	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys			
	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp			
	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu			
	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys			
	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe			
	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu			
	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu			
	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser			
	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala			
	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro			
	290	295	300
Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro Tyr Met Ala			

305 310 315 320
 Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val Pro Ile Asp
 325 330 335
 Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg Glu Met Ile
 340 345 350
 Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr Leu Asn Thr
 355 360 365
 Glu Leu
 370

<210> 105
 <211> 445
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (20)..(430)

<400> 105
 aacaacaatt tcaagagac atg gca ggc aaa ggt gga aaa gga ctc gta gct 52
 Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala
 1 5 10
 gcg aag acg atg gct gct aac aag gac aaa gac aag gac aag aag aaa 100
 Ala Lys Thr Met Ala Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys
 15 20 25
 ccc atc tct cgc tct gct cgt gct ggt att cag ttt cca gtt gga cga 148
 Pro Ile Ser Arg Ser Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg
 30 35 40
 att cac agg caa ctg aag acc cga gtc tcg gca cat ggc aga gtt ggt 196
 Ile His Arg Gln Leu Lys Thr Arg Val Ser Ala His Gly Arg Val Gly
 45 50 55
 gcc act gca gcc gtc tac aca gct tca atc ctg gag tat ctg aca gca 244
 Ala Thr Ala Ala Val Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala
 60 65 70 75
 gag gtt ctt gag ttg gct ggg aat gcg agc aag gat ctc aaa gtg aag 292
 Glu Val Leu Glu Leu Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys
 80 85 90
 agg ata acg cca agg cat ctg cag ttg gcg att aga gga gat gag gag 340
 Arg Ile Thr Pro Arg His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu
 95 100 105
 ctg gac aca ctc atc aag gga acg att gct gga ggt ggt gtg atc cct 388
 Leu Asp Thr Leu Ile Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro
 110 115 120

cac atc cac aag tct ctc atc aac aaa acc acc aag gag tga 430
 His Ile His Lys Ser Leu Ile Asn Lys Thr Thr Lys Glu
 125 130 135

tgtgtagctt tttat 445

<210> 106
 <211> 136
 <212> PRT
 <213> Arabidopsis thaliana

<400> 106
 Met Ala Gly Lys Gly Gly Lys Gly Leu Val Ala Ala Lys Thr Met Ala
 1 5 10 15
 Ala Asn Lys Asp Lys Asp Lys Asp Lys Lys Lys Pro Ile Ser Arg Ser
 20 25 30
 Ala Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
 35 40 45
 Lys Thr Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
 50 55 60
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
 65 70 75 80
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
 85 90 95
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
 100 105 110
 Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
 115 120 125
 Leu Ile Asn Lys Thr Thr Lys Glu
 130 135

<210> 107
 <211> 930
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (14)..(916)

<400> 107
 gcctccttgg ctt atg tac tta cca aaa cgt ggc aat ttg ttc gaa ctc 49
 Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu
 1 5 10

tat gat cca ttg cat cag aag atg tac aca ttg aat cta cct gag ctt	97
Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
45 50 55 60	
ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
110 115 120	
aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
tgg gat ttt agt tac acc tat tta ctg cca tgt cct tat atc tcg gat	529
Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
 240 245 250

ctt cgt ttt aat gtc aag cgt tgt gta tca tat tcg ctt gat gaa gag 817
 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
 255 260 265

agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865
 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
 270 275 280

att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913
 Ile Glu Asn Leu Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
 285 290 295 300

tga agataaaaagt aatg 930

<210> 108

<211> 300

<212> PRT

<213> Arabidopsis thaliana

<400> 108

Met Tyr Leu Pro Lys Arg Gly Asn Leu Phe Glu Leu Tyr Asp Pro Leu
 1 5 10 15

His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu Ala Lys Ser Thr
 20 25 30

Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg Lys Thr Ile Ser
 35 40 45

Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
 50 55 60

Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
 65 70 75 80

Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
 85 90 95

Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr Glu Trp Val Thr
 100 105 110

Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
 115 120 125

Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
 130 135 140

Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
 145 150 155 160

Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
 165 170 175

Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
 180 185 190
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His
 195 200 205
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp
 210 215 220
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
 225 230 235 240
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn
 245 250 255
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
 260 265 270
 Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro Ile Glu Asn Leu
 275 280 285
 Trp Ile Arg Pro Pro Lys Lys Ala Val Asp Phe Met
 290 295 300

<210> 109
 <211> 2640
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (145)..(981)

<220>
 <221> CDS
 <222> (1439)..(1727)

<220>
 <221> CDS
 <222> (1817)..(2126)

<220>
 <221> CDS
 <222> (2204)..(2330)

<220>
 <221> CDS
 <222> (2405)..(2518)

<400> 109
 tccacggcta caaaagaaca ttctcgacat acacaaaaaa attcgaaatt tcgagaactc 60
 tcttgtgcct tcttcttcat cttctctgt ttttaaaaat gcaatcaagc agattctcac 120

gataccta ¹ aaa ccaa ⁵ atccaa ttca atg gcg gaa gaa gca aaa tcc aaa gga	171
Met Ala Glu Glu Ala Lys Ser Lys Gly	
aac gca gct ttc tct tcc ggc gat tac gcc acc gca ata acc cat ttc	219
Asn Ala Ala Phe Ser Ser Gly Asp Tyr Ala Thr Ala Ile Thr His Phe	
10 15 20 25	
aca gaa gca atc aac ctt tca cca acc aat cac atc ctc tac tca aac	267
Thr Glu Ala Ile Asn Leu Ser Pro Thr Asn His Ile Leu Tyr Ser Asn	
30 35 40	
aga tcc gct tct tac gct tct ctc cac cgt tac gaa gaa gct tta tca	315
Arg Ser Ala Ser Tyr Ala Ser Leu His Arg Tyr Glu Glu Ala Leu Ser	
45 50 55	
gac gcg aag aag act ata gag ctt aaa cct gat tgg tct aaa gga tat	363
Asp Ala Lys Lys Thr Ile Glu Leu Lys Pro Asp Trp Ser Lys Gly Tyr	
60 65 70	
agc cga tta ggt gct gcg ttt att gga ttg tcc aag ttt gat gaa gcg	411
Ser Arg Leu Gly Ala Ala Phe Ile Gly Leu Ser Lys Phe Asp Glu Ala	
75 80 85	
gtt gat tcg tat aag aaa gga tta gag att gat ccg agt aat gag atg	459
Val Asp Ser Tyr Lys Lys Gly Leu Glu Ile Asp Pro Ser Asn Glu Met	
90 95 100 105	
ctt aaa tcg gga tta gct gat gct tcg aga tct agg gtt tcg tca aag	507
Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser Lys	
110 115 120	
tcg aat cct ttt gtt gat gcg ttt caa ggg aag gag atg tgg gag aag	555
Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu Lys	
125 130 135	
ttg acg gcg gat ccg ggg act agg gtt tat ttg gag cag gat gat ttt	603
Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp Phe	
140 145 150	
gtt aag acg atg aag gag att cag agg aac cct aat aat ctt aat ttg	651
Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn Leu	
155 160 165	
tat atg aag gat aag aga gtt atg aag gct tta ggg gtt ttg ttg aat	699
Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu Asn	
170 175 180 185	
gtg aag ttt ggt gga tct agt ggt gaa gat act gag atg aag gag gct	747
Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu Ala	
190 195 200	
gat gag agg aaa gag cct gaa ccg gag atg gaa cct atg gag ttg acg	795
Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu Thr	
205 210 215	
gag gag gag agg cag aag aag gag aga aag gag aag gct ttg aag gag	843

Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys Glu
 220 225 230
 aaa ggg gaa gga aat gtt gct tat aag aag aag gat ttt ggg aga gct 891
 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala
 235 240 245
 gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser
 250 255 260 265
 tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys
 270 275
 gtattaagtc ttataacttgg cttaaaagtt aaacctttag gtactttaag attaaggagg 1041
 agatcttggg ttcttgaagt agcttatctg tttagtatag cttgtcacta gttagtacat 1101
 ttgtgatgac cttgatgggt ttgataact ttcactctgct tcttgttga gatttaagag 1161
 ttttgaactt aagttttcac ttgtgctgaa agtagtttagc tttagatgag gtagaaattt 1221
 aggggtttatg gcttcatgat ggagtttatt cacttgttct gtagaagtgg ttatctttat 1281
 tattactgga atcaattaat cttcaagtat cctgagtggg tcaattccat tgggtctatgt 1341
 gttcttgcac tagtcttgtt taattaacag ttggttcac tggatcttac tgtatcttgt 1401
 gtgatgtttt acttcatttc tcaaatgaaa ttatcag tac gag gag tgc att gaa 1456
 Tyr Glu Glu Cys Ile Glu
 280 285
 gac tgt gac aag gct gtt gaa aga ggc aga gaa ctt cgt tct gac ttc 1504
 Asp Cys Asp Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe
 290 295 300
 aag atg ata gca aga gct ctg act aga aaa gga tct gct cta gtg aaa 1552
 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys
 305 310 315
 atg gcg aga tgc tcg aaa gac ttt gag cct gcg att gag act ttc cag 1600
 Met Ala Arg Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln
 320 325 330
 aaa gct ctt aca gag cat cgt aat cca gat aca ttg aag aaa ctg aac 1648
 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn
 335 340 345
 gat gct gag aaa gtc aag aaa gag ctg gag caa cag gag tac ttt gat 1696
 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp
 350 355 360 365
 cct acg ata gcc gag gag gag cga gag aaa g gtatatatac tgatcctcag 1747
 Pro Thr Ile Ala Glu Glu Glu Arg Glu Lys G
 370 375

203

Val Gln Val Arg
555

gaagatgttt ccaaattttc actgcgttct tttgggcttt tgttaaactg atgaaactct 2618
gatttggttt gggtcattgtt tg 2640

<210> 110
<211> 558
<212> PRT
<213> Arabidopsis thaliana

<400> 110
Met Ala Glu Glu Ala Lys Ser Lys Gly Asn Ala Ala Phe Ser Ser Gly
1 5 10 15
Asp Tyr Ala Thr Ala Ile Thr His Phe Thr Glu Ala Ile Asn Leu Ser
20 25 30
Pro Thr Asn His Ile Leu Tyr Ser Asn Arg Ser Ala Ser Tyr Ala Ser
35 40 45
Leu His Arg Tyr Glu Glu Ala Leu Ser Asp Ala Lys Lys Thr Ile Glu
50 55 60
Leu Lys Pro Asp Trp Ser Lys Gly Tyr Ser Arg Leu Gly Ala Ala Phe
65 70 75 80
Ile Gly Leu Ser Lys Phe Asp Glu Ala Val Asp Ser Tyr Lys Lys Gly
85 90 95
Leu Glu Ile Asp Pro Ser Asn Glu Met Leu Lys Ser Gly Leu Ala Asp
100 105 110
Ala Ser Arg Ser Arg Val Ser Ser Lys Ser Asn Pro Phe Val Asp Ala
115 120 125
Phe Gln Gly Lys Glu Met Trp Glu Lys Leu Thr Ala Asp Pro Gly Thr
130 135 140
Arg Val Tyr Leu Glu Gln Asp Asp Phe Val Lys Thr Met Lys Glu Ile
145 150 155 160
Gln Arg Asn Pro Asn Asn Leu Asn Leu Tyr Met Lys Asp Lys Arg Val
165 170 175
Met Lys Ala Leu Gly Val Leu Leu Asn Val Lys Phe Gly Gly Ser Ser
180 185 190
Gly Glu Asp Thr Glu Met Lys Glu Ala Asp Glu Arg Lys Glu Pro Glu
195 200 205
Pro Glu Met Glu Pro Met Glu Leu Thr Glu Glu Glu Arg Gln Lys Lys
210 215 220
Glu Arg Lys Glu Lys Ala Leu Lys Glu Lys Gly Glu Gly Asn Val Ala

225		230		235		240
Tyr Lys Lys Lys Asp Phe Gly Arg Ala Val Glu His Tyr Thr Lys Ala						
		245		250		255
Met Glu Leu Asp Asp Glu Asp Ile Ser Tyr Leu Thr Asn Arg Ala Ala						
		260		265		270
Val Tyr Leu Glu Met Gly Lys Tyr Glu Glu Cys Ile Glu Asp Cys Asp						
		275		280		285
Lys Ala Val Glu Arg Gly Arg Glu Leu Arg Ser Asp Phe Lys Met Ile						
		290		295		300
Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys Met Ala Arg						
		305		310		315
Cys Ser Lys Asp Phe Glu Pro Ala Ile Glu Thr Phe Gln Lys Ala Leu						
		325		330		335
Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn Asp Ala Glu						
		340		345		350
Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp Pro Thr Ile						
		355		360		365
Ala Glu Glu Glu Arg Glu Lys Gly Asn Gly Phe Phe Lys Glu Gln Lys						
		370		375		380
Tyr Pro Glu Ala Val Lys His Tyr Ser Glu Ala Ile Lys Arg Asn Pro						
		385		390		395
Asn Asp Val Arg Ala Tyr Ser Asn Arg Ala Ala Cys Tyr Thr Lys Leu						
		405		410		415
Gly Ala Leu Pro Glu Gly Leu Lys Asp Ala Glu Lys Cys Ile Glu Leu						
		420		425		430
Asp Pro Ser Phe Thr Lys Gly Tyr Ser Arg Lys Gly Ala Ile Gln Phe						
		435		440		445
Phe Met Lys Glu Tyr Asp Lys Ala Met Glu Thr Tyr Gln Glu Gly Leu						
		450		455		460
Lys His Asp Pro Lys Asn Gln Glu Phe Leu Asp Gly Val Arg Arg Cys						
		465		470		475
Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu Glu						
		485		490		495
Leu Lys Glu Arg Gln Ala Lys Ala Met Gln Asp Pro Glu Val Gln Asn						
		500		505		510
Ile Leu Ser Asp Pro Val Met Arg Gln Val Leu Val Asp Phe Gln Glu						
		515		520		525
Asn Pro Lys Ala Ala Gln Glu His Met Lys Asn Pro Met Val Met Asn						

530

535

540

Lys Ile Gln Lys Leu Val Ser Ala Gly Ile Val Gln Val Arg
 545 550 555

<210> 111

<211> 1560

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (130)..(265)

<220>

<221> CDS

<222> (386)..(515)

<220>

<221> CDS

<222> (622)..(1480)

<400> 111

tatataaacc tcacacacgc attatcatatc accatcctcc tcattctctt catcatcaac 60

ataagagaga gagaagaaaa aaagaattac aattaataag aacaagatca agaatcaaga 120

atcaagaaa atg gga aga gca ccg tgt tgt gat aag gcc aac gtg aag aaa 171

Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
 1 5 10

ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219

Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu
 15 20 25 30

aat agt ggc aca gga ggc aac tgg att gct ttg cct cag aaa att g 265

Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G
 35 40 45

gtatgtatta cttaaaactc acttttgatt taaaattggc actgagagtt tccaaatagt 325

actttgagac cgtggctcgtg tttaaatttgt gtgttgatga tatttattta catggtatag 385

gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432

ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr
 50 55 60

ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac 480

Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn
 65 70 75

atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525

Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar
 80 85

cttagagact cactatgtat ctttgtttaa ttctag g tgg tct ata att gct gca 640
g Trp Ser Ile Ile Ala Ala
90 95

agg ctg aag aag aag ctt ctg aac aaa caa agg aaa gag ttc caa gaa 736
Arg Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu
115 120 125

caa gga caa ggt caa agt aat ggt agt acg gat ctt tat ctt aac aac 832
Gln Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn
145 150 155

cat cat caa ata cct ctt gga atg atg gaa cca aca agc tgt aac tac 928
His His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr
180 185 190

ctc aag aac atg gtc aag att gaa gaa gaa cag gaa agg aca aac cct 1024
Leu Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro
210 215 220

tct cag ctt ttg tta gat ccc aat tac tat ctg gga tca gga ggg gga . 1120
Ser Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly
240 245 250 255

cca aac aca agt agt gat caa cat cca agt caa cag caa gag att ctt 1216
Pro Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu
275 280 285

caa tgg ttt ggg agc agt aac ttt cag aca gaa gca atc aac gat atg 1264
Gln Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met
290 295 300

ttc ata aac aac aac aac aac ata gtg aat ctt gag acc atc gag aac 1312
 Phe Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn
 305 310 315

aca aaa gtc tat gga gac gcc tca gta gcc gga gcc gct gtc cga gca 1360
 Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala
 320 325 330 335

gct ttg ggc gga ggg aca acg agt aca tcg gcg gat caa agt aca ata 1408
 Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile
 340 345 350

agt tgg gag gat ata act tct cta gtt aat tcc gaa gat gca agt tac 1456
 Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr
 355 360 365

ttc aat gcg cca aat cat gtg taa cattttgttt aaaactttat ttgtacttaa 1510
 Phe Asn Ala Pro Asn His Val
 370 375

atacataaag aggggttttc tattttgtat aaatctgtgt ctttagggag 1560

<210> 112

<211> 374

<212> PRT

<213> Arabidopsis thaliana

<400> 112

Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys Gly Pro
 1 5 10 15

Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu Asn Ser
 20 25 30

Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile Gly Leu Arg
 35 40 45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
 50 55 60

Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys
 65 70 75 80

Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln
 85 90 95

Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg
 100 105 110

Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala
 115 120 125

Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln
 130 135 140

Gly Gln Gly Gln Ser Asn Gly Ser Thr Asp Leu Tyr Leu Asn Asn Met
 145 150 155 160
 Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro His
 165 170 175
 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr
 180 185 190
 Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu
 195 200 205
 Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp
 210 215 220
 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser
 225 230 235 240
 Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly
 245 250 255
 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro
 260 265 270
 Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu Gln
 275 280 285
 Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met Phe
 290 295 300
 Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn Thr
 305 310 315 320
 Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala
 325 330 335
 Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile Ser
 340 345 350
 Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr Phe
 355 360 365
 Asn Ala Pro Asn His Val
 370

<210> 113
 <211> 3790
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (38)..(1597)

<220>

<221> CDS
 <222> (1717)..(1943)

<220>
 <221> CDS
 <222> (2052)..(2384)

<220>
 <221> CDS
 <222> (2468)..(2714)

<220>
 <221> CDS
 <222> (2800)..(2928)

<220>
 <221> CDS
 <222> (3020)..(3203)

<220>
 <221> CDS
 <222> (3532)..(3773)

<400> 113
 ttgtatggtt cggtgttact gatagattac ttaagct atg gtt tgg ttt aga atc 55
 Met Val Trp Phe Arg Ile
 1 5

ggt tct tct gtg gca aag ctt gcc ata aga agg aca ctg tct cag tct 103
 Gly Ser Ser Val Ala Lys Leu Ala Ile Arg Arg Thr Leu Ser Gln Ser
 10 15 20

cgt tgt ggt tca tat gcc act aga aca agg gtt ttg cct tgt caa acc 151
 Arg Cys Gly Ser Tyr Ala Thr Arg Thr Arg Val Leu Pro Cys Gln Thr
 25 30 35

aga tgt ttt cac tct aca ata ctc aaa tca aag gca gag tct gct gca 199
 Arg Cys Phe His Ser Thr Ile Leu Lys Ser Lys Ala Glu Ser Ala Ala
 40 45 50

cct gtt cca cgt cct gtc cca ctt tct aag cta act gat agc ttc tta 247
 Pro Val Pro Arg Pro Val Pro Leu Ser Lys Leu Thr Asp Ser Phe Leu
 55 60 65 70

gat gga aca agc agt gtg tat cta gag gag tta caa aga gct tgg gag 295
 Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu Leu Gln Arg Ala Trp Glu
 75 80 85

gct gat ccc aac agt gtt gat gag tcg tgg gat aac ttt ttt agg aat 343
 Ala Asp Pro Asn Ser Val Asp Glu Ser Trp Asp Asn Phe Phe Arg Asn
 90 95 100

ttt gtg ggt cag gct tct aca tcg cct ggt atc tcg ggg caa acc att 391
 Phe Val Gly Gln Ala Ser Thr Ser Pro Gly Ile Ser Gly Gln Thr Ile
 105 110 115

caa gaa agc atg cgt ttg ttg ttg cta gtt aga gct tac cag gtt aat 439

Gln	Glu	Ser	Met	Arg	Leu	Leu	Leu	Leu	Val	Arg	Ala	Tyr	Gln	Val	Asn		
120						125					130						
ggc	cac	atg	aag	gcc	aag	ctt	gat	cct	tta	ggt	cta	gag	aag	aga	gag	487	
Gly	His	Met	Lys	Ala	Lys	Leu	Asp	Pro	Leu	Gly	Leu	Glu	Lys	Arg	Glu		
135					140					145					150		
att	cca	gag	gat	ctc	acg	cca	ggt	ctt	tat	ggg	ttt	act	gag	gct	gat	535	
Ile	Pro	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Tyr	Gly	Phe	Thr	Glu	Ala	Asp		
				155					160					165			
ctt	gat	cgg	gaa	ttc	ttt	ctg	ggt	gta	tgg	agg	atg	tcg	ggt	ttt	ctc	583	
Leu	Asp	Arg	Glu	Phe	Phe	Leu	Gly	Val	Trp	Arg	Met	Ser	Gly	Phe	Leu		
			170					175					180				
tct	gag	aac	cgc	ccg	gtt	caa	aca	ctg	agg	tcg	ata	ctg	tcg	agg	ctt	631	
Ser	Glu	Asn	Arg	Pro	Val	Gln	Leu	Arg	Ser	Ile	Leu	Ser	Arg	Leu			
		185					190					195					
gag	caa	gct	tac	tgt	ggg	act	ata	ggg	tat	gag	tac	atg	cac	att	gct	679	
Glu	Gln	Ala	Tyr	Cys	Gly	Thr	Ile	Gly	Tyr	Glu	Tyr	Met	His	Ile	Ala		
	200					205					210						
gat	agg	gat	aaa	tgt	aac	tgg	ttg	aga	gac	aag	atc	gag	acc	cca	act	727	
Asp	Arg	Asp	Lys	Cys	Asn	Trp	Leu	Arg	Asp	Lys	Ile	Glu	Thr	Pro	Thr		
215					220					225					230		
cct	cga	cag	tac	aat	agt	gag	cgt	cgg	atg	gtt	att	tat	gat	agg	ctt	775	
Pro	Arg	Gln	Tyr	Asn	Ser	Glu	Arg	Arg	Met	Val	Ile	Tyr	Asp	Arg	Leu		
				235					240					245			
acc	tgg	agc	aca	cag	ttt	gag	aat	ttc	ttg	gct	act	aag	tgg	acc	acg	823	
Thr	Trp	Ser	Thr	Gln	Phe	Glu	Asn	Phe	Leu	Ala	Thr	Lys	Trp	Thr	Thr		
			250					255					260				
gct	aaa	agg	ttt	gga	ctg	gaa	ggt	gct	gaa	tct	ttg	att	cct	ggc	atg	871	
Ala	Lys	Arg	Phe	Gly	Leu	Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Gly	Met		
		265					270					275					
aag	gag	atg	ttc	gat	agg	tct	gca	gat	ctc	ggg	gta	gag	aac	ata	gtt	919	
Lys	Glu	Met	Phe	Asp	Arg	Ser	Ala	Asp	Leu	Gly	Val	Glu	Asn	Ile	Val		
	280					285					290						
atc	ggt	atg	ccc	cat	agg	ggt	cga	ctt	aat	gtt	ttg	ggt	aat	gtt	gtt	967	
Ile	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Gly	Asn	Val	Val		
295					300					305					310		
aga	aaa	cct	cta	cgc	caa	ata	ttc	agc	gag	ttt	agc	ggt	ggt	act	agg	1015	
Arg	Lys	Pro	Leu	Arg	Gln	Ile	Phe	Ser	Glu	Phe	Ser	Gly	Gly	Thr	Arg		
				315					320					325			
cca	gta	gat	gaa	gtt	ggg	ctt	tac	acc	gga	aca	ggt	gat	gtg	aaa	tac	1063	
Pro	Val	Asp	Glu	Val	Gly	Leu	Tyr	Thr	Gly	Thr	Gly	Asp	Val	Lys	Tyr		
			330					335					340				
cac	ttg	ggt	aca	tct	tat	gat	cgt	cca	act	aga	gga	ggc	aaa	cat	ctc	1111	
His	Leu	Gly	Thr	Ser	Tyr	Asp	Arg	Pro	Thr	Arg	Gly	Gly	Lys	His	Leu		

345	350	355	
cac ttg tct ttg gta gca aat ccc agt cac ttg gaa gca gta gat cct His Leu Ser Leu Val Ala Asn Pro Ser His Leu Glu Ala Val Asp Pro 360 365 370			1159
ggt gtg ata ggt aaa acc aga gcg aaa caa tat tac acg aaa gac gag Val Val Ile Gly Lys Thr Arg Ala Lys Gln Tyr Tyr Thr Lys Asp Glu 375 380 385 390			1207
aac aga aca aag aac atg ggt att ttg atc cat ggg gat ggt agc ttt Asn Arg Thr Lys Asn Met Gly Ile Leu Ile His Gly Asp Gly Ser Phe 395 400 405			1255
gcc gga caa gga gtg gtg tat gaa act ctc cat ctt agt gca ctt cct Ala Gly Gln Val Val Tyr Glu Thr Leu His Leu Ser Ala Leu Pro 410 415 420			1303
aac tac tgt acc ggt gga aca gtg cac att gtg gtg aat aat caa gtg Asn Tyr Cys Thr Gly Gly Thr Val His Ile Val Val Asn Asn Gln Val 425 430 435			1351
gct ttc aca acc gat ccc agg gaa gga agg tct tca cag tat tgc act Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg Ser Ser Gln Tyr Cys Thr 440 445 450			1399
gat gtt gca aag gct ttg agc gcc cca att ttc cat gtc aat gca gat Asp Val Ala Lys Ala Leu Ser Ala Pro Ile Phe His Val Asn Ala Asp 455 460 465 470			1447
gac att gaa gca gta gtg cat gct tgt gag ctt gct gct gag tgg cgc Asp Ile Glu Ala Val Val His Ala Cys Glu Leu Ala Ala Glu Trp Arg 475 480 485			1495
cag acg ttc cat tct gat gtt gtt gtt gat tta gta tgc tac cgt cgc Gln Thr Phe His Ser Asp Val Val Val Asp Leu Val Cys Tyr Arg Arg 490 495 500			1543
ttt ggg cat aac gag ata gac gaa ccg tca ttc aca caa cca aaa atg Phe Gly His Asn Glu Ile Asp Glu Pro Ser Phe Thr Gln Pro Lys Met 505 510 515			1591
tac aag gtctggctat tatatcatcc atctctgtga aataatctaa taaccaattc Tyr Lys 520			1647
aagtttccat ttcatacttt tcttgacttt tttttttggt taaaaacgga tggtacttgt			1707
tggtgatag gtg ata cgc agt cat ccc tcg tca ctt caa atc tac cag gag Val Ile Arg Ser His Pro Ser Ser Leu Gln Ile Tyr Gln Glu 525 530			1758
aag ctc ttg caa tct gga cag gta acc caa gaa gat att gat aag att Lys Leu Leu Gln Ser Gly Gln Val Thr Gln Glu Asp Ile Asp Lys Ile 535 540 545 550			1806
caa aag aaa gta agc tct atc ctc aat gaa gaa tat gag gca agt aaa			1854

Gln Lys Lys Val Ser Ser Ile Leu Asn Glu Glu Tyr Glu Ala Ser Lys
 555 560 565
 gat tat att cca caa aaa cgt gac tgg ctg gca agt cac tgg act gga 1902
 Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu Ala Ser His Trp Thr Gly
 570 575 580
 ttc aag tct ccg gag cag att tct agg att cga aac acc gg gtaaaaaaca 1953
 Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile Arg Asn Thr Gl
 585 590 595
 tttttatttc atttagtttg tcaatgcctt ttggcctttt ttcttttctt tttcaatgta 2013
 acattttgct ggaaaactat tcccttggtc ttttgcag a gtg aag cca gag att 2067
 y Val Lys Pro Glu Ile
 600
 ttg aag aat gtg gga aag gca atc tca acc ttc cct gag aac ttt aag 2115
 Leu Lys Asn Val Gly Lys Ala Ile Ser Thr Phe Pro Glu Asn Phe Lys
 605 610 615
 cca cac aga gga gtt aaa aga gtt tat gaa caa cgt gct caa atg att 2163
 Pro His Arg Gly Val Lys Arg Val Tyr Glu Gln Arg Ala Gln Met Ile
 620 625 630
 gaa tcg gga gaa ggc att gac tgg gga ctt gga gaa gca ctt gct ttt 2211
 Glu Ser Gly Glu Gly Ile Asp Trp Gly Leu Gly Glu Ala Leu Ala Phe
 635 640 645
 gct aca ctg gtt gtg gaa ggg aac cat gtt cgg cta agt ggt caa gat 2259
 Ala Thr Leu Val Val Glu Gly Asn His Val Arg Leu Ser Gly Gln Asp
 650 655 660 665
 gtt gaa aga gga act ttc agt cat aga cac tca gtg ctt cat gat caa 2307
 Val Glu Arg Gly Thr Phe Ser His Arg His Ser Val Leu His Asp Gln
 670 675 680
 gaa acc ggg gag gaa tat tgt ccc ctc gat cac cta atc aaa aac caa 2355
 Glu Thr Gly Glu Glu Tyr Cys Pro Leu Asp His Leu Ile Lys Asn Gln
 685 690 695
 gac cct gaa atg ttc act gtc agc aac ag gtatgcattt ttttttaac 2404
 Asp Pro Glu Met Phe Thr Val Ser Asn Se
 700 705
 tctagagatg ataaccactc ttcaattggt ttacatgat ctttacgttg tttgtgatg 2464
 cag c tcc ctt tca gaa ttt ggt gtt ctc ggt ttc gaa ctg ggt tat tcg 2513
 r Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu Gly Tyr Se
 710 715 720
 atg gaa aat ccc aat tct ctg gtg ata tgg gaa gct cag ttt gga gac 2561
 r Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln Phe Gly As
 725 730 735
 ttt gct aat ggc gca caa gtt atg ttt gat cag ttc ata agc agt ggg 2609
 p Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile Ser Ser Gl

740 745 750
 gaa gcc aaa tgg ctc cgt caa act ggt cta gta gtt tta ctt cct cat 2657
 y Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu Leu Pro Hi
 755 760 765 770
 gga tat gat ggt cag ggt cct gaa cat tcc agt gga aga ttg gaa cgt 2705
 s Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg Leu Glu Ar
 775 780 785
 ttc ctt cag gtatattata tgaccgatac ttaccgttaa gattctctcc 2754
 g Phe Leu Gln
 actttttgta tttgtttccc tctcatttga aaattttaac tgcag atg agt gat gac 2811
 Met Ser Asp As
 790
 aat cct tac gtt atc cct gag atg gac cca act ctt cga aag cag att 2859
 p Asn Pro Tyr Val Ile Pro Glu Met Asp Pro Thr Leu Arg Lys Gln Il
 795 800 805
 caa gaa tgt aat tgg caa gtt gtt aat gtt act aca cct gcc aac tat 2907
 e Gln Glu Cys Asn Trp Gln Val Val Asn Val Thr Thr Pro Ala Asn Ty
 810 815 820 825
 ttc cat gtt ctg cgt cgg cag gtaaaatata ttttatccc aagttcgtaa 2958
 r Phe His Val Leu Arg Arg Gln
 830
 aatgttgta cttaattttc gtattcttca cactcacatg cttgatata tccatttgca 3018
 g ata cac agg gac ttt cgc aag cct ctt ata gtg atg gcc ccc aaa aac 3067
 Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys As
 835 840 845
 ttg ctt cgt cac aaa cag tgt gta tct aat ctc tgc gaa ttc gat gat 3115
 n Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp As
 850 855 860
 gtt aaa gga cat cct gga ttt gac aag caa gga act cga ttt aaa cgg 3163
 p Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys Ar
 865 870 875 880
 ttg atc aaa gat caa agt ggc cac tct gat ctt gaa gaa g gtatcagacg 3213
 g Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu A
 885 890
 tctagtcctc tgctctggga aggtataaaa aaaaagatcc actttttccg tcattaacta 3273
 acaaagtcc cacattctga aatttaatac tttaaatgtc aatgaatcag gtctactatg 3333
 agcttgacga agagcgaaag aagtctgaaa caaaggatgt agccatttgc agagtagagc 3393
 agctttgccc atttccatat gatctcatcc aaagagaact aaagcgatat ccaagtaggc 3453
 gtcgaaaact caagtttgtg ttcaatagtt ttggttgatt atggaattct ttgaaacttt 3513

```
<210> 114
<211> 947
<212> PRT
<213> Arabidopsis thaliana
```

```

<400> 114
Met Val Trp Phe Arg Ile Gly Ser Ser Val Ala Lys Leu Ala Ile Arg
  1              5              10              15

Arg Thr Leu Ser Gln Ser Arg Cys Gly Ser Tyr Ala Thr Arg Thr Arg
              20              25              30

Val Leu Pro Cys Gln Thr Arg Cys Phe His Ser Thr Ile Leu Lys Ser
      35              40              45

Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
  50              55              60

Leu Thr Asp Ser Phe Leu Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu
  65              70              75              80

Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
              85              90              95

Asp Asn Phe Phe Arg Asn Phe Val Gly Gln Ala Ser Thr Ser Pro Gly
      100              105              110

Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Leu Val
      115              120              125

Arg Ala Tyr Gln Val Asn Gly His Met Lys Ala Lys Leu Asp Pro Leu
  130              135              140

```

Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr
 145 150 155 160
 Gly Phe Thr Glu Ala Asp Leu Asp Arg Glu Phe Phe Leu Gly Val Trp
 165 170 175
 Arg Met Ser Gly Phe Leu Ser Glu Asn Arg Pro Val Gln Thr Leu Arg
 180 185 190
 Ser Ile Leu Ser Arg Leu Glu Gln Ala Tyr Cys Gly Thr Ile Gly Tyr
 195 200 205
 Glu Tyr Met His Ile Ala Asp Arg Asp Lys Cys Asn Trp Leu Arg Asp
 210 215 220
 Lys Ile Glu Thr Pro Thr Pro Arg Gln Tyr Asn Ser Glu Arg Arg Met
 225 230 235 240
 Val Ile Tyr Asp Arg Leu Thr Trp Ser Thr Gln Phe Glu Asn Phe Leu
 245 250 255
 Ala Thr Lys Trp Thr Thr Ala Lys Arg Phe Gly Leu Glu Gly Ala Glu
 260 265 270
 Ser Leu Ile Pro Gly Met Lys Glu Met Phe Asp Arg Ser Ala Asp Leu
 275 280 285
 Gly Val Glu Asn Ile Val Ile Gly Met Pro His Arg Gly Arg Leu Asn
 290 295 300
 Val Leu Gly Asn Val Val Arg Lys Pro Leu Arg Gln Ile Phe Ser Glu
 305 310 315 320
 Phe Ser Gly Gly Thr Arg Pro Val Asp Glu Val Gly Leu Tyr Thr Gly
 325 330 335
 Thr Gly Asp Val Lys Tyr His Leu Gly Thr Ser Tyr Asp Arg Pro Thr
 340 345 350
 Arg Gly Gly Lys His Leu His Leu Ser Leu Val Ala Asn Pro Ser His
 355 360 365
 Leu Glu Ala Val Asp Pro Val Val Ile Gly Lys Thr Arg Ala Lys Gln
 370 375 380
 Tyr Tyr Thr Lys Asp Glu Asn Arg Thr Lys Asn Met Gly Ile Leu Ile
 385 390 395 400
 His Gly Asp Gly Ser Phe Ala Gly Gln Gly Val Val Tyr Glu Thr Leu
 405 410 415
 His Leu Ser Ala Leu Pro Asn Tyr Cys Thr Gly Gly Thr Val His Ile
 420 425 430
 Val Val Asn Asn Gln Val Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg
 435 440 445

Ser Ser Gln Tyr Cys Thr Asp Val Ala Lys Ala Leu Ser Ala Pro Ile
 450 455 460
 Phe His Val Asn Ala Asp Asp Ile Glu Ala Val Val His Ala Cys Glu
 465 470 475 480
 Leu Ala Ala Glu Trp Arg Gln Thr Phe His Ser Asp Val Val Val Asp
 485 490 495
 Leu Val Cys Tyr Arg Arg Phe Gly His Asn Glu Ile Asp Glu Pro Ser
 500 505 510
 Phe Thr Gln Pro Lys Met Tyr Lys Val Ile Arg Ser His Pro Ser Ser
 515 520 525
 Leu Gln Ile Tyr Gln Glu Lys Leu Leu Gln Ser Gly Gln Val Thr Gln
 530 535 540
 Glu Asp Ile Asp Lys Ile Gln Lys Lys Val Ser Ser Ile Leu Asn Glu
 545 550 555 560
 Glu Tyr Glu Ala Ser Lys Asp Tyr Ile Pro Gln Lys Arg Asp Trp Leu
 565 570 575
 Ala Ser His Trp Thr Gly Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile
 580 585 590
 Arg Asn Thr Gly Val Lys Pro Glu Ile Leu Lys Asn Val Gly Lys Ala
 595 600 605
 Ile Ser Thr Phe Pro Glu Asn Phe Lys Pro His Arg Gly Val Lys Arg
 610 615 620
 Val Tyr Glu Gln Arg Ala Gln Met Ile Glu Ser Gly Glu Gly Ile Asp
 625 630 635 640
 Trp Gly Leu Gly Glu Ala Leu Ala Phe Ala Thr Leu Val Val Glu Gly
 645 650 655
 Asn His Val Arg Leu Ser Gly Gln Asp Val Glu Arg Gly Thr Phe Ser
 660 665 670
 His Arg His Ser Val Leu His Asp Gln Glu Thr Gly Glu Glu Tyr Cys
 675 680 685
 Pro Leu Asp His Leu Ile Lys Asn Gln Asp Pro Glu Met Phe Thr Val
 690 695 700
 Ser Asn Ser Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu
 705 710 715 720
 Gly Tyr Ser Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln
 725 730 735
 Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile
 740 745 750

Ser Ser Gy Glu Ala Lys Trp Leu Arg Gln Thr Gly Leu Val Val Leu
 755 760 765
 Leu Pro Hs Gly Tyr Asp Gly Gln Gly Pro Glu His Ser Ser Gly Arg
 770 775 780
 Leu Glu Ag Phe Leu Gln Met Ser Asp Asp Asn Pro Tyr Val Ile Pro
 785 790 795
 Glu Met Asp Pro Thr Leu Arg Lys Gln Ile Gln Glu Cys Asn Trp Gln
 800 805 810
 Val Val Asn Val Thr Thr Pro Ala Asn Trp Phe His Val Leu Arg Arg
 815 820 825
 Gln Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys
 830 835 840
 Asn Leu Leu Arg His Lys Gln Cys Val Ser Asn Leu Ser Glu Phe Asp
 845 850 855
 Asp Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys
 860 865 870
 Arg Leu Ile Lys Asp Gln Ser Gly His Ser Asp Leu Glu Glu
 875 880 885
 Asp Ala Glu Ile Val Trp Cys Gln Glu Glu Pro Met Asn Met Gly Gly
 890 895 900
 Tyr Gln Tyr Ile Ala Leu Arg Leu Cys Thr Ala Met Lys Ala Leu Gln
 905 910 915
 Arg Gly Asn Phe Asn Asp Ile Lys Tyr Val Gly Arg Leu Pro Ser Ala
 920 925 930
 Ala Thr Ala Thr Gly Phe Tyr Gln Leu His Val Lys Glu Gln Thr Asp
 935
 Leu Val Lys Lys Ala Leu Gln
 Pro Asp Pro Ile Thr Pro Val Ile Pro

<210> 115
 <211> 1200
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (25)..(151)

<220>
 <221> CDS

<222> (257)..(357)

<220>

<221> CDS

<222> (465)..(662)

<220>

<221> CDS

<222> (783)..(1166)

<400> 115

```

tgcattttta ctctcttgac gcta atg ttc att cgg gtt tcc gct cga ccc 51
Met Phe Ile Arg Val Ser Ala Arg Pro
1 5

gcg aca ttc gtc gag gat ttc aaa gcc gcc tgg tgg gaa tct cac atc 99
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
10 15 20 25

cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc 147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
30 35 40

act g gtacaccaac gccacagtta tatttttaaa cggaacatt ttgaaattaa 201
Thr G

tggtgttttt atgtaatata ctctcactgt acatgttcat atttgtcttt taaag ga 258
ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg 306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
45 50 55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc 354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
60 65 70 75

tac gtaagtctat cattttactc cactagtttt gaaattttac acattcacac 407
Tyr

aataaaaaat aacattttct tgaaacacta acggtcaaatt cattgatatg tctatag 464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc 512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
80 85 90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt 560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
95 100 105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac 608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
110 115 120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac 656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
125 130 135 140

```

att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc 712
Ile Val

aaaacaaaaa atcaccattt actgttttaa aaaaccttag tttaacgtgg ggttgttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
145 150 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta 869
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
160 165 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
220 225 230 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat 1109
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys
255 260 265

cgt gct tga aaataattgc atacgtacgt tgcaatgatc atgt 1200
Arg Ala
270

<210> 116
<211> 269
<212> PRT
<213> Arabidopsis thaliana

<400> 116
Met Phe Ile Arg Val Ser Ala Arg Pro Ala Thr Phe Val Glu Asp Phe
1 5 10 15
Lys Ala Ala Trp Ser Glu Ser His Ile Arg Gln Met Glu Asp Gly Lys
20 25 30
Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser
35 40 45

Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile
 50 55 60
 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
 65 70 75 80
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
 85 90 95
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
 100 105 110
 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp
 115 120 125
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
 130 135 140
 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn
 145 150 155 160
 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp
 165 170 175
 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp
 180 185 190
 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
 195 200 205
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
 210 215 220
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg
 225 230 235 240
 Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp
 245 250 255
 Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys Arg Ala
 260 265

<210> 117
 <211> 1399
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (25)..(1386)

<400> 117

```

aacacaaacc gaggttttag aaac atg gcg tct aag gta atc tct gcc aca      51
                        Met Ala Ser Lys Val Ile Ser Ala Thr
                          1                      5

atc cgc aga acc cta acc aaa cca cac ggc act ttt tcc cgg tgt cgc      99
Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
 10                      15                      20                      25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa      147
Tyr Leu Ser Thr Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
                      30                      35                      40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta      195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
                      45                      50                      55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg      243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
                      60                      65                      70

aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat      291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
 75                      80                      85

ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag      339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
 90                      95                      100                      105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc      387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
                      110                      115                      120

ggt gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt      435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
                      125                      130                      135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag      483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
                      140                      145                      150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta      531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
                      155                      160                      165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg      579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
                      170                      175                      180                      185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg      627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
                      190                      195                      200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att      675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
                      205                      210                      215

```

tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile 220 225 230	723
ggg aag ata cct gtt gat gtt aag aag tgg aat gtt gct ttg atg tct Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser 235 240 245	771
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr 250 255 260 265	819
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly 270 275 280	867
ggg cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile 285 290 295	915
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr 300 305 310	963
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val 315 320 325	1011
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg 330 335 340 345	1059
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser 350 355 360	1107
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys 365 370 375	1155
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val 380 385 390	1203
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe 395 400 405	1251
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln 410 415 420 425	1299
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu 430 435 440	1347
ggg atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

Gly Ile Asp Ile Lys Asn Ile Gln Trp Ser Gln His
 445 450

cca

1399

<210> 118

<211> 453

<212> PRT

<213> Arabidopsis thaliana

<400> 118

Met Ala Ser Lys Val Ile Ser Ala Thr Ile Arg Arg Thr Leu Thr Lys
 1 5 10 15

Pro His Gly Thr Phe Ser Arg Cys Arg Tyr Leu Ser Thr Ala Ala Ala
 20 25 30

Ala Thr Glu Val Asn Tyr Glu Asp Glu Ser Ile Met Met Lys Gly Val
 35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro
 50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu
 65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu
 85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala
 100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn
 115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His
 130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg
 145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr
 165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp
 180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val
 195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro
 210 215 220

Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val
 225 230 235 240

```
<210> 119
<211> 3180
<212> DNA
<213> Arabidopsis thaliana
```

```
<220>
<221> CDS
<222> (8)..(1781)

<220>
<221> CDS
<222> (1833)..(2609)
```

<220>

<221> CDS

<222> (2697)..(3076)

<400> 119

```

caacacg atg ctc acc aat act aat ctc ttc ttc ttt ctc tct tta ctt 49
      Met Leu Thr Asn Thr Asn Leu Phe Phe Phe Leu Ser Leu Leu
          1              5              10

ctt ctt tct tgt ttt ctc caa gtt tct tcc aat gga gac gct gag ata 97
Leu Leu Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile
15              20              25              30

ttg agt aga gtt aaa aag acc cga ctt ttc gac ccc gat gga aat tta 145
Leu Ser Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu
              35              40              45

caa gat tgg gtc ata acc gga gat aat cgg agt cca tgt aat tgg acg 193
Gln Asp Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr
              50              55              60

gga atc aca tgc cac atc aga aaa ggt agc tcc ctc gcc gtc act acc 241
Gly Ile Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr
              65              70              75

att gat ctc tcc ggc tat aat atc tcc ggt ggc ttt ccc tac gga ttc 289
Ile Asp Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe
              80              85              90

tgt cgt atc cgt aca ctc atc aac atc act ctt tct caa aac aat ctc 337
Cys Arg Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu
95              100              105              110

aat ggt acg att gat tct gct cct ctc tcc ctc tgt tct aaa ctt cag 385
Asn Gly Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln
              115              120              125

aat ttg att ctc aat caa aac aac ttc tcc ggt aaa tta ccg gaa ttc 433
Asn Leu Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe
              130              135              140

tca ccg gag ttt cgt aaa tta cga gtc ctc gaa ttg gaa tca aac ctc 481
Ser Pro Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu
              145              150              155

ttc acc ggt gag att cct caa agt tac ggg aga ctc act gct ctg caa 529
Phe Thr Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln
              160              165              170

gtt ctg aat ctt aat ggt aac ccg ctc agt gga atc gtt ccg gcg ttt 577
Val Leu Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe
175              180              185              190

ttg ggt tat ctg act gag tta act cgt ctt gat ctc gct tac atc agt 625
Leu Gly Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser
              195              200              205

```

ttt gat cct agt ccg att cca tca acc ttg ggg aac ttg tcg aat ctg Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu 210 215 220	673
act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp 225 230 235	721
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn 240 245 250	769
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val 255 260 265 270	817
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu 275 280 285	865
agt atc gga aat tta acc gaa ttg agg aat ttt gat gtc tcg cag aat Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn 290 295 300	913
aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile 305 310 315	961
tct ttc aat ctc aat gat aat ttc ttc acc gga gga tta cca gat gtc Ser Phe Asn Leu Asn Asp Asn Phe Phe Thr Gly Glu Leu Pro Asp Val 320 325 330	1009
gta gct ttg aat cct aat ctc gtt gaa ttc aaa atc ttc aac aac agt Val Ala Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser 335 340 345 350	1057
ttc acg ggg acg tta cca agg aat ctc ggg aaa ttc tca gaa atc tct Phe Thr Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser 355 360 365	1105
gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr 370 375 380	1153
ttg tgc tac aga aga aaa ctt cag aag att atc acc ttc agc aat caa Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln 385 390 395	1201
tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn 400 405 410	1249
tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg 415 420 425 430	1297
ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa	1345

Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln	
435 440 445	
tta caa ggt tgc att cct cct tgc att tcc aaa gct cgt cat cta tct	1393
Leu Gln Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser	
450 455 460	
cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa	1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
465 470 475	
ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt	1489
Leu Cys Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser	
480 485 490	
ttc tta gga tca att ccg tct tgc atc aac aaa ttg aag aat cta gag	1537
Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu	
495 500 505 510	
aga gta gag atg cag gag aac atg ctc gac ggc gag att ccg agt tca	1585
Arg Val Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser	
515 520 525	
gtg agt tgc tgc acc gag tta acc gaa tta aat ctc tcc aac aac cgt	1633
Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg	
530 535 540	
tta cga ggc ggg ata cca ccg gaa ctc ggt gat tta ccg gtt tta aac	1681
Leu Arg Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn	
545 550 555	
tac ctg gat ctc tct aac aac caa ctc acc ggt gag att ccg gcg gag	1729
Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
560 565 570	
ctg ttg agg ctc aag ctt aat caa ttc aac gtc tcc gat aac aaa ctc	1777
Leu Leu Arg Leu Lys Leu Asn Gln Phe Asn Val Ser Asp Asn Lys Leu	
575 580 585 590	
tat g gtaagattcc ttctggattt cagcaagata tttttcgacc cagtttctta g gt	1834
Tyr G ly	
aac ccg aat ctc tgt gcc cca aat ttg gat ccg att aga cct tgc cga	1882
Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
595 600 605	
tcc aaa ccg gaa acc ccg tac att ctc cca atc tca atc ctc tgc atc	1930
Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg	1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
tta ttc aag aga aaa ccg aaa ccg acc aac aaa ata acc atc ttc cag	2026
Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln	
645 650 655	

cgg gtc ggg ttc acg gag gaa gac ata tac ccg caa tta aca gaa gat Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp 660 665 670	2074
aac ata att ggg tcg ggc ggg tcg ggt ttg gtt tat aga gtg aaa ctc Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu 675 680 685	2122
aaa tca ggt caa acg ctt gcg gtg aag aaa ctc tgg gga gaa acg ggt Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly 690 695 700	2170
caa aaa acg gaa tct gaa tct gtt ttt cga tcc gaa gta gag acg ttg Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu 705 710 715 720	2218
ggt cgg gtc aga cat gga aac atc gtg aaa ctt ctt atg tgc tgc aac Gly Arg Val Arg His Gly Asn Ile Val Lys Leu Leu Met Cys Cys Asn 725 730 735	2266
ggc gag gag ttt cgg ttc tta gtg tac gag ttc atg gaa aac ggc agc Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser 740 745 750	2314
tta ggt gac gtt ttg cat tcg gag aaa gaa cat cgt gcc gtt tct cca Leu Gly Asp Val Leu His Ser Glu Lys Glu His Arg Ala Val Ser Pro 755 760 765	2362
ctt gat tgg acg aca cga ttt tcg atc gcg gtt ggt gct gct caa gga Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly 770 775 780	2410
ctt tct tat cta cat cat gac tct gtt ccg cct att gtt cac cgt gac Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp 785 790 795 800	2458
gtc aaa agc aat aat ata ttg ttg gac cat gag atg aag cca cgt gtc Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val 805 810 815	2506
gcc gat ttc ggt tta gct aaa ccg ttg aag aga gaa gac aat gat ggt Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly 820 825 830	2554
gtc tcc gat gtt tca atg tct tgt gtt gct gga tcc tac ggc tac att Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile 835 840 845	2602
gct ccg g gttcgaattc ttagctctac aatatcaaat cgtaaacc ctatacgcaa Ala Pro G 850	2659
gcgttttagt aacattactg ttcttctgtg gatgcag aa tat ggt tat acg tca lu Tyr Gly Tyr Thr Ser 855	2713

aaa gtg aat gag aag agc gat gtc tat agc ttc ggg gtg gtt tta ctc 2761
 Lys Val Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu
 860 865 870

gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat 2809
 Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn
 875 880 885

aag gac att gtt aag ttt gca atg gaa gca gct ttg tgt tac cct tct 2857
 Lys Asp Ile Val Lys Phe Ala Met Glu Ala Ala Leu Cys Tyr Pro Ser
 890 895 900

cca tca gca gaa gac gga gcc atg aat caa gat tca ctt gga aac tat 2905
 Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr
 905 910 915 920

cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga 2953
 Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg
 925 930 935

gag tat gaa gag ata gag aaa gtt ctt gac gtt gca ttg ctc tgt acg 3001
 Glu Tyr Glu Glu Ile Glu Lys Val Leu Asp Val Ala Leu Leu Cys Thr
 940 945 950

tcg tct ttt cct atc aac agg ccg acc atg agg aaa gta gta gag ttg 3049
 Ser Ser Phe Pro Ile Asn Arg Pro Thr Met Arg Lys Val Val Glu Leu
 955 960 965

ctt aaa gag aag aaa tca cta gag tga tattaatcct aggcctttaa 3096
 Leu Lys Glu Lys Lys Ser Leu Glu
 970 975

ttattaggct tctataatgt acaaaatccg actaggattg ttactcatta ttatagccat 3156

aggttggaact ttgctttaa gttt 3180

<210> 120
 <211> 976
 <212> PRT
 <213> Arabidopsis thaliana

<400> 120
 Met Leu Thr Asn Thr Asn Leu Phe Phe Phe Leu Ser Leu Leu Leu Leu
 1 5 10 15

Ser Cys Phe Leu Gln Val Ser Ser Asn Gly Asp Ala Glu Ile Leu Ser
 20 25 30

Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu Gln Asp
 35 40 45

Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile
 50 55 60

Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp
 65 70 75 80

Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe Cys Arg
 85 90 95
 Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu Asn Gly
 100 105 110
 Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln Asn Leu
 115 120 125
 Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe Ser Pro
 130 135 140
 Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu Phe Thr
 145 150 155 160
 Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln Val Leu
 165 170 175
 Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe Leu Gly
 180 185 190
 Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser Phe Asp
 195 200 205
 Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu Thr Asp
 210 215 220
 Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp Ser Ile
 225 230 235 240
 Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn Ser Leu
 245 250 255
 Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val Tyr Gln
 260 265 270
 Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu Ser Ile
 275 280 285
 Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn Asn Leu
 290 295 300
 Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile Ser Phe
 305 310 315 320
 Asn Leu Asn Asp Asn Phe Phe Thr Gly Gly Leu Pro Asp Val Val Ala
 325 330 335
 Leu Asn Pro Asn Leu Val Glu Phe Lys Ile Phe Asn Asn Ser Phe Thr
 340 345 350
 Gly Thr Leu Pro Arg Asn Leu Gly Lys Phe Ser Glu Ile Ser Glu Phe
 355 360 365
 Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr Leu Cys
 370 375 380

Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln Leu Ser
 385 390 395 400
 Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn Tyr Ile
 405 410 415
 Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg Phe Trp
 420 425 430
 Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln Leu Gln
 435 440 445
 Gly Ser Ile Pro Pro Ser Ile Ser Lys Ala Arg His Leu Ser Gln Leu
 450 455 460
 Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys Leu Cys
 465 470 475 480
 Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser Phe Leu
 485 490 495
 Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu Arg Val
 500 505 510
 Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser Val Ser
 515 520 525
 Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg Leu Arg
 530 535 540
 Gly Gly Ile Pro Pro Glu Leu Gly Asp Leu Pro Val Leu Asn Tyr Leu
 545 550 555 560
 Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu Leu Leu
 565 570 575
 Arg Leu Lys Leu Asn Gln Phe Asn Val Ser Asp Asn Lys Leu Tyr Gly
 580 585 590
 Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg
 595 600 605
 Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile
 610 615 620
 Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro
 625 630 635 640
 Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln
 645 650 655
 Arg Val Gly Phe Thr Glu Glu Asp Ile Tyr Pro Gln Leu Thr Glu Asp
 660 665 670
 Asn Ile Ile Gly Ser Gly Gly Ser Gly Leu Val Tyr Arg Val Lys Leu
 675 680 685

Lys Ser Gly Gln Thr Leu Ala Val Lys Lys Leu Trp Gly Glu Thr Gly
 690 695 700
 Gln Lys Thr Glu Ser Glu Ser Val Phe Arg Ser Glu Val Glu Thr Leu
 705 710 715 720
 Gly Arg Val Arg His Gly Asn Ile Val Lys Leu Leu Met Cys Cys Asn
 725 730 735
 Gly Glu Glu Phe Arg Phe Leu Val Tyr Glu Phe Met Glu Asn Gly Ser
 740 745 750
 Leu Gly Asp Val Leu His Ser Glu Lys Glu His Arg Ala Val Ser Pro
 755 760 765
 Leu Asp Trp Thr Thr Arg Phe Ser Ile Ala Val Gly Ala Ala Gln Gly
 770 775 780
 Leu Ser Tyr Leu His His Asp Ser Val Pro Pro Ile Val His Arg Asp
 785 790 795 800
 Val Lys Ser Asn Asn Ile Leu Leu Asp His Glu Met Lys Pro Arg Val
 805 810 815
 Ala Asp Phe Gly Leu Ala Lys Pro Leu Lys Arg Glu Asp Asn Asp Gly
 820 825 830
 Val Ser Asp Val Ser Met Ser Cys Val Ala Gly Ser Tyr Gly Tyr Ile
 835 840 845
 Ala Pro Glu Tyr Gly Tyr Thr Ser Lys Val Asn Glu Lys Ser Asp Val
 850 855 860
 Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys Arg Pro
 865 870 875 880
 Asn Asp Ser Ser Phe Gly Glu Asn Lys Asp Ile Val Lys Phe Ala Met
 885 890 895
 Glu Ala Ala Leu Cys Tyr Pro Ser Pro Ser Ala Glu Asp Gly Ala Met
 900 905 910
 Asn Gln Asp Ser Leu Gly Asn Tyr Arg Asp Leu Ser Lys Leu Val Asp
 915 920 925
 Pro Lys Met Lys Leu Ser Thr Arg Glu Tyr Glu Glu Ile Glu Lys Val
 930 935 940
 Leu Asp Val Ala Leu Leu Cys Thr Ser Ser Phe Pro Ile Asn Arg Pro
 945 950 955 960
 Thr Met Arg Lys Val Val Glu Leu Leu Lys Glu Lys Lys Ser Leu Glu
 965 970 975

<210> 121
 <211> 731
 <212> DNA
 <213> Arabidopsis thaliana

<400> 121
 aagtcgagta tgattgtccg tacgtgctcg acggtgcgac cgtacgtacc ctggcagtcg 60
 ccctgacgca acttcgaatc tgccctgcgc cctgctctct ctatggcagt actgctact 120
 tcgacgagca ggagctgaag ctgactataa cgtgcctggt cgaaaagcat gccagcccat 180
 gaaaaaggag atcgagaacg gtatctcgga cttcggcgag gacgggtccg ggaacgtcga 240
 ttctgagaag tccgtgcaaa tcggtacggc gcggaacggc gagcgccacg cagcgacga 300
 ggtcataaac gaaacccgcc tggtcggcgc acgccaacc gggacgataa cctgcaacag 360
 cctaaaaacgc ccggccgagg agctaggcca gggggcggac ccggaggaga tcccgggaac 420
 ccgcgacgag gccgacaggc agggcgacgg cgagaccaag aacgaacgtg ccgtcagctg 480
 tagaccggac gggcgaccca tccagcctga ccgcttggac ccgtaccgtg tgcctgaaat 540
 gcctgaattc gcctgcctt ggatgcctgc tctgaaatgc tcgcctgttg cctgaattcg 600
 ctctgaaatc cgttcccccg cctccgcagc tcgtgaccgt ccgaaccgtc cgaaccctgc 660
 aaaaaaagcc tcgaaaaaaa aaaaaggctc aaaaaaaaaa aaaaaacagt ccaaaaaaaa 720
 aaacgcctcg c 731

<210> 122
 <211> 21
 <212> DNA
 <213> Artificial sequence

<400> 122
 aaaaaacaca tacaggaatt c

<210> 123
 <211> 21
 <212> DNA
 <213> Artificial sequence

<400> 123
 agttagctag ctgagctcga g